

Genforce version 5.1.6
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nm nucleotide - nucleotide search, using sw model

Run on: August 13, 2003, 14:05:48 : Search time 00:00:45 seconds

(with/out updates/sec)
1419/743 hits from 1011 updates/sec

Title: US-10-009-962-1

Perfect score: 28

Sequence: 1 CCGTCGACAACTTCTTAACTTCACATCA

Search table:

IDENTITY_N90
Gapop 10.0 : Gapext 1.0

Searches: 2888711 seqs, 2045413386 positions

Total number of hits satisfying chosen parameters: 577742

Minimum seq length: 0

Maximum seq length: 200000000

Post Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Genbank:
1: gb_ba:
2: gb_ba:
3: gb_in:
4: gb_om:
5: gb_om:
6: gb_om:
7: gb_om:
8: gb_pl:
9: gb_pl:
10: gb_pl:
11: gb_pl:
12: gb_pl:
13: gb_pl:
14: gb_pl:
15: gb_pl:
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37: gb_pl:
38: gb_pl:
39: gb_pl:
40: gb_pl:
41: gb_pl:

Prob. No. is the number of results predicted by chosen database

Score distribution table of results of the search of the database
and is ordered by analysis of the total score distribution

2/2888711

Result No.	Score	Match	Length	Database	Accession	Source	Organism
1	20	100%	10	Genbank	AF000001	Human	Homo sapiens
2	20	100%	10	Genbank	AF000002	Human	Homo sapiens
3	20	100%	10	Genbank	AF000003	Human	Homo sapiens
4	20	100%	10	Genbank	AF000004	Human	Homo sapiens
5	20	100%	10	Genbank	AF000005	Human	Homo sapiens
6	20	100%	10	Genbank	AF000006	Human	Homo sapiens
7	20	100%	10	Genbank	AF000007	Human	Homo sapiens
8	20	100%	10	Genbank	AF000008	Human	Homo sapiens
9	20	100%	10	Genbank	AF000009	Human	Homo sapiens
10	20	100%	10	Genbank	AF000010	Human	Homo sapiens
11	20	100%	10	Genbank	AF000011	Human	Homo sapiens
12	20	100%	10	Genbank	AF000012	Human	Homo sapiens
13	20	100%	10	Genbank	AF000013	Human	Homo sapiens
14	20	100%	10	Genbank	AF000014	Human	Homo sapiens
15	20	100%	10	Genbank	AF000015	Human	Homo sapiens
16	20	100%	10	Genbank	AF000016	Human	Homo sapiens
17	20	100%	10	Genbank	AF000017	Human	Homo sapiens
18	20	100%	10	Genbank	AF000018	Human	Homo sapiens
19	20	100%	10	Genbank	AF000019	Human	Homo sapiens
20	20	100%	10	Genbank	AF000020	Human	Homo sapiens
21	20	100%	10	Genbank	AF000021	Human	Homo sapiens
22	20	100%	10	Genbank	AF000022	Human	Homo sapiens
23	20	100%	10	Genbank	AF000023	Human	Homo sapiens
24	20	100%	10	Genbank	AF000024	Human	Homo sapiens
25	20	100%	10	Genbank	AF000025	Human	Homo sapiens
26	20	100%	10	Genbank	AF000026	Human	Homo sapiens
27	20	100%	10	Genbank	AF000027	Human	Homo sapiens
28	20	100%	10	Genbank	AF000028	Human	Homo sapiens
29	20	100%	10	Genbank	AF000029	Human	Homo sapiens
30	20	100%	10	Genbank	AF000030	Human	Homo sapiens
31	20	100%	10	Genbank	AF000031	Human	Homo sapiens
32	20	100%	10	Genbank	AF000032	Human	Homo sapiens
33	20	100%	10	Genbank	AF000033	Human	Homo sapiens
34	20	100%	10	Genbank	AF000034	Human	Homo sapiens
35	20	100%	10	Genbank	AF000035	Human	Homo sapiens
36	20	100%	10	Genbank	AF000036	Human	Homo sapiens
37	20	100%	10	Genbank	AF000037	Human	Homo sapiens
38	20	100%	10	Genbank	AF000038	Human	Homo sapiens
39	20	100%	10	Genbank	AF000039	Human	Homo sapiens
40	20	100%	10	Genbank	AF000040	Human	Homo sapiens
41	20	100%	10	Genbank	AF000041	Human	Homo sapiens
42	20	100%	10	Genbank	AF000042	Human	Homo sapiens
43	20	100%	10	Genbank	AF000043	Human	Homo sapiens
44	20	100%	10	Genbank	AF000044	Human	Homo sapiens
45	20	100%	10	Genbank	AF000045	Human	Homo sapiens

2/2888711

RESULT 1	Accession	Source	Organism
AF000001	Human	Homo sapiens	
AF000002	Human	Homo sapiens	
AF000003	Human	Homo sapiens	
AF000004	Human	Homo sapiens	
AF000005	Human	Homo sapiens	
AF000006	Human	Homo sapiens	
AF000007	Human	Homo sapiens	
AF000008	Human	Homo sapiens	
AF000009	Human	Homo sapiens	
AF000010	Human	Homo sapiens	
AF000011	Human	Homo sapiens	
AF000012	Human	Homo sapiens	
AF000013	Human	Homo sapiens	
AF000014	Human	Homo sapiens	
AF000015	Human	Homo sapiens	
AF000016	Human	Homo sapiens	
AF000017	Human	Homo sapiens	
AF000018	Human	Homo sapiens	
AF000019	Human	Homo sapiens	
AF000020	Human	Homo sapiens	
AF000021	Human	Homo sapiens	
AF000022	Human	Homo sapiens	
AF000023	Human	Homo sapiens	
AF000024	Human	Homo sapiens	
AF000025	Human	Homo sapiens	
AF000026	Human	Homo sapiens	
AF000027	Human	Homo sapiens	
AF000028	Human	Homo sapiens	
AF000029	Human	Homo sapiens	
AF000030	Human	Homo sapiens	
AF000031	Human	Homo sapiens	
AF000032	Human	Homo sapiens	
AF000033	Human	Homo sapiens	
AF000034	Human	Homo sapiens	
AF000035	Human	Homo sapiens	
AF000036	Human	Homo sapiens	
AF000037	Human	Homo sapiens	
AF000038	Human	Homo sapiens	
AF000039	Human	Homo sapiens	
AF000040	Human	Homo sapiens	
AF000041	Human	Homo sapiens	
AF000042	Human	Homo sapiens	
AF000043	Human	Homo sapiens	
AF000044	Human	Homo sapiens	
AF000045	Human	Homo sapiens	

TITLE Direct Submission
REFERENCE 2 (bases 1 to 219645)
AUTHORS Morley, K.C.
TITLE Direct Submission
REFERENCE Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
AUTHORS 3 (bases 1 to 219645)
TITLE Rat Genome Sequencing Consortium
REFERENCE Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 19, 2002 this sequence version replaced H1962713.
 The sequence in this assembly is a combination of BAC-based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.bcm.tmc.edu/atlantis/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a "contig scaffold"). Within each scaffold, individual sequence readings are ordered and oriented, and separated by sized gaps filled with "N"s. The contig scaffolds may extend beyond the ends of the clones and there may be sequence contigs within a contig scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Genome Center
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hsc-help@bcm.tmc.edu
Project Information
Center project name: HGHS
Center clone name: CH240-265021

Summary Statistics
Assembly program: Phrap version 0.990329
Consensus quality: 106840 bases at least Q40
Consensus quality: 190576 bases at least Q40
Consensus quality: 192814 bases at least Q20
Estimated insert size: 193452; sum of contigs estimation
Quality coverage: 4x to Q20 bases; sum of contigs estimation

NOTE: Estimated insert size may differ from sequence length.
NOTE: This is a "working draft" sequence. It currently consists of 3 contigs. The true order of the clones is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of "N"s. Both the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 216412: contig of 216412 bp in length
 * 216413 216412: gap of unknown length
 * 216413 216412: gap of 1260 bp in length
 * 216413 216412: gap of unknown length
 * 216413 216412: contig of 1864 bp in length

FEATURES
SOURCE
 /organism "Rattus norvegicus"
 /cell_type "embryo RNA"
 /db_name "GenBank"

FASTA COUNT 55574 a 42247 c 12177 g 5115 t 25192 others
ORIGIN
 Query Match 70.08; Score 19.6; DB: 2; Length 219645
 Identical Similarity 84.69; Ident. No. 4,560;2
 Mismatches 22; Conservativity 0; Mismatches 1; Subst. 2; Gaps 0

RESULT 14
ACCESSION AC110955.7
DEFINITION Rat H1962713
FEATURES
ACCESSION AC110955.7
VERSION 1
AUTHORS Morley, K.C.
SOURCE Rat Genome Sequencing Consortium
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS

TITLE Direct Submission
REFERENCE 2 (bases 1 to 219645)
AUTHORS Morley, K.C.
TITLE Direct Submission
REFERENCE Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
AUTHORS 3 (bases 1 to 219645)
TITLE Rat Genome Sequencing Consortium
REFERENCE Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 19, 2002 this sequence version replaced H1962713.
 The sequence in this assembly is a combination of BAC-based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.bcm.tmc.edu/atlantis/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a "contig scaffold"). Within each scaffold, individual sequence readings are ordered and oriented, and separated by sized gaps filled with "N"s. The contig scaffolds may extend beyond the ends of the clones and there may be sequence contigs within a contig scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Cambridge version 5.1.4.
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OM multiple - nucleic search, using sw model

RUN ON: August 13, 2003, 19:05:48 ; Secured, 1 min 30.00, 417.5 sec 40.00

[illegible]

Title: US-10-009-962-2

Sequence: 1 CCGTGGACCTTAAGAACTCTCTGGAGG 2F

Scoring table: IDENTITY_NUC

Searched: 288871 seqs, 20454813306 residues

Total number of hits satisfying chosen parameters: 5777422.

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Listing first 45 summaries

Fatalitas :

GenEmb: 1: qb_ba: *
2: qb_hlg: *
3: qb_in: *
4: qb_com: *
5: qb_ov: *
6: qb_pat: *
7: qb_ph: *
8: qb_pl: *
9: qb_pr: *
10: qb_ro: *
11: qb_sts: *
12: qb_sy: *
13: qb_un: *
14: qb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mn: *
20: em_com: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_in: *
32: em_hlg_of_ho: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rod: *
36: em_hlg_mam: *
37: em_hlg_vr: *
38: em_sy: *
39: em_hlgo_hum: *
40: em_hlgo_mus: *
41: em_hlgo_of_ho: *

Pred. No. is the number of results predicted by chance to have a

Case	Model	Method	Results
1	Model 1	Method 1	Results 1
2	Model 2	Method 2	Results 2
3	Model 3	Method 3	Results 3
4	Model 4	Method 4	Results 4
5	Model 5	Method 5	Results 5
6	Model 6	Method 6	Results 6
7	Model 7	Method 7	Results 7
8	Model 8	Method 8	Results 8
9	Model 9	Method 9	Results 9
10	Model 10	Method 10	Results 10
11	Model 11	Method 11	Results 11
12	Model 12	Method 12	Results 12
13	Model 13	Method 13	Results 13
14	Model 14	Method 14	Results 14
15	Model 15	Method 15	Results 15
16	Model 16	Method 16	Results 16
17	Model 17	Method 17	Results 17
18	Model 18	Method 18	Results 18
19	Model 19	Method 19	Results 19
20	Model 20	Method 20	Results 20
21	Model 21	Method 21	Results 21
22	Model 22	Method 22	Results 22
23	Model 23	Method 23	Results 23
24	Model 24	Method 24	Results 24
25	Model 25	Method 25	Results 25
26	Model 26	Method 26	Results 26
27	Model 27	Method 27	Results 27
28	Model 28	Method 28	Results 28
29	Model 29	Method 29	Results 29
30	Model 30	Method 30	Results 30
31	Model 31	Method 31	Results 31
32	Model 32	Method 32	Results 32
33	Model 33	Method 33	Results 33
34	Model 34	Method 34	Results 34
35	Model 35	Method 35	Results 35
36	Model 36	Method 36	Results 36
37	Model 37	Method 37	Results 37
38	Model 38	Method 38	Results 38
39	Model 39	Method 39	Results 39
40	Model 40	Method 40	Results 40
41	Model 41	Method 41	Results 41
42	Model 42	Method 42	Results 42
43	Model 43	Method 43	Results 43
44	Model 44	Method 44	Results 44
45	Model 45	Method 45	Results 45
46	Model 46	Method 46	Results 46
47	Model 47	Method 47	Results 47
48	Model 48	Method 48	Results 48
49	Model 49	Method 49	Results 49
50	Model 50	Method 50	Results 50
51	Model 51	Method 51	Results 51
52	Model 52	Method 52	Results 52
53	Model 53	Method 53	Results 53
54	Model 54	Method 54	Results 54
55	Model 55	Method 55	Results 55
56	Model 56	Method 56	Results 56
57	Model 57	Method 57	Results 57
58	Model 58	Method 58	Results 58
59	Model 59	Method 59	Results 59
60	Model 60	Method 60	Results 60
61	Model 61	Method 61	Results 61
62	Model 62	Method 62	Results 62
63	Model 63	Method 63	Results 63
64	Model 64	Method 64	Results 64
65	Model 65	Method 65	Results 65
66	Model 66	Method 66	Results 66
67	Model 67	Method 67	Results 67
68	Model 68	Method 68	Results 68
69	Model 69	Method 69	Results 69
70	Model 70	Method 70	Results 70
71	Model 71	Method 71	Results 71
72	Model 72	Method 72	Results 72
73	Model 73	Method 73	Results 73
74	Model 74	Method 74	Results 74
75	Model 75	Method 75	Results 75
76	Model 76	Method 76	Results 76
77	Model 77	Method 77	Results 77
78	Model 78	Method 78	Results 78
79	Model 79	Method 79	Results 79
80	Model 80	Method 80	Results 80
81	Model 81	Method 81	Results 81
82	Model 82	Method 82	Results 82
83	Model 83	Method 83	Results 83
84	Model 84	Method 84	Results 84
85	Model 85	Method 85	Results 85
86	Model 86	Method 86	Results 86
87	Model 87	Method 87	Results 87
88	Model 88	Method 88	Results 88
89	Model 89	Method 89	Results 89
90	Model 90	Method 90	Results 90
91	Model 91	Method 91	

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 \mathcal{F}_{100}

Result No.	Score	Country	Match	Score	Opp.
1	20.5	USA	8	17.5	A1750001
2	20.5	USA	7	17.5	A1750001
3	19.5	USA	6	15.5	A1750001
4	19.5	USA	5	17.5	A1750001
5	19.5	USA	4	17.5	A1750001
6	19.5	USA	3	17.5	A1750001
7	19.5	USA	2	17.5	A1750001
8	19.5	USA	1	17.5	A1750001
9	19.5	USA	0	17.5	A1750001
10	19.5	USA	0	17.5	A1750001
11	19.5	USA	0	17.5	A1750001
12	19.5	USA	0	17.5	A1750001
13	19.5	USA	0	17.5	A1750001
14	19.5	USA	0	17.5	A1750001
15	19.5	USA	0	17.5	A1750001
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43	19.5	USA	0	17.5	A1750001
44	19.5	USA	0	17.5	A1750001
45	19.5	USA	0	17.5	A1750001

[illegible]

Query Match 76.0% Score 19.64 Lb 2 Length 19768
 Best Local Similarity 84.6% Pred. No. 3,964,421
 Matches 227 Conserved 0 Mismatches 12 Indels 2 Gap 1

UY 1 CCGTCAGCTAAGACCTTCGAG 26
 ||| ||||| ||||| |||||
 Db 11856 CCGCGCTCTTCAGACCTTCGAG 11841

RESULT 9
 AT110K17 109016 bp DNA linear JUN 2001 JAN 2002
 LOCUS Arabidopsis thaliana DNA chromosome 4, BAC clone 11 K17.
 DEFINITION AT112977
 ACCESSION AL112977.1 GI:6434224
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Equisetophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis;
 1
 BECK, V., KRAMER, J., BROCK, B., ALLEN, R., MAYER, K., MAYOR, F., QUOTER, F., and SALAMONHA, M.,
 LEMKE, K., MAYOR, F., QUOTER, F., and SALAMONHA, M.,
 unpublished
 2 (bases 1 to 109016)
 EU Arabidopsis sequencing project.
 DIRECT SUBMISSION
 Submitted (19-JAN-1999) MIPS, at the Max Planck Institut fuer
 Biochemie, Am Klopfersfeld 19a, D-82152 Martinsried, Germany.
 Lemke/Mayer Biochemie/Mayer/MIPS Biochemie/Mayer project
 Coordinator: Marcel Salamonha and Francis Quoter, Groupement
 d'Interet Public, Centre National de Sequencage, GENOSCOPE, 2 rue
 Gaston Crémieux, 91006 Evry-Courcouronnes, France
 http://www.genoscope.cns.fr
 COMMENT Information on polymorphisms of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 4, 4
 and 5 can be viewed at: <http://www.11.k17.b4.112977>
 Location/Qualifiers
 1..109016
 /organism "Arabidopsis thaliana"
 /mol_type "genomic DNA"
 /project "Arabidopsis thaliana"
 /db_xref "Genbank:2992"
 /chromosome "4"
 1..5127
 /note "Overlap to BAC T1508, please refer to Acc. no.
 FMBL:AL049660 for analysis and annotation"
 3113..6400
 /gene "T10K17.10"
 complement(join(3113..5577,4386..4374,5574..5572,5577,5669..5782,5855..6400))
 /gene "T10K17.10"
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 /gene "T10K17.10"
 /note "Similarity to several hypothetical proteins
 Arabidopsis thaliana"
 /codon_start 1
 /product "putative protein"
 /protein_id "CA867608.1"
 /db_xref "GI:6729523"
 /feature (1) "MULTICISTEADYME REPTILININ INTERACTING
 G-TOG-LIPIDATION TOXICITY-INDUCED PROTEIN INTERACTING
 MECHANISM-INDUCED TOXICITY-INDUCED PROTEIN INTERACTING
 ENDOPLASMIC RETICULUM-INDUCED TOXICITY-INDUCED PROTEIN
 ERANKINAWAY TOXICITY-INDUCED TOXICITY-INDUCED PROTEIN
 RIDENOTILASIN-INDUCED TOXICITY-INDUCED PROTEIN
 GINCEV-INDUCED TOXICITY-INDUCED PROTEIN"
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GenCore version 5.1.6
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on nucleic - nucleic search, using sw model

Run on: August 13, 2003, 15:05:48 ; Search time 749.185 seconds
(with about 410000000)

(without alignment)
1419.743 Million words updated/Sec

Title:	US-10-009-462-3
Page:	36

Sequence: 1 GCATTATCACTTAGCACTTCCACCC 25

Scoring table: IDENTITY_NUC

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters. 67774022

Maximum IP seq length: 2000000000

Post-processing:	Minimum Match	0%	100%
Maximum Match	100%		

listing first. 45 summaries

Database :

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2:	qb_hiq *
3:	qb_lm *
4:	qb_on *
5:	qb_ov *
6:	qb_pal *
7:	qb_ph *
8:	qb_pl *
9:	qb_pre *
10:	qb_ro *
11:	qb_scs *
12:	qb_sy *
13:	qb_un *
14:	qb_vl *
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16:	cm_hum *
17:	cm_jun *
18:	cm_jin *
19:	cm_jun *
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23:	cm_pal *
24:	cm_ph *
25:	cm_pl *
26:	cm_ro *
27:	cm_scs *
28:	cm_un *
29:	cm_vl *
30:	em_hq_jun *
31:	em_hq_jun *
32:	em_hq_other *
33:	em_hq_mus *
34:	em_hq_pl *
35:	em_hq_ro *
36:	em_hq_un *
37:	em_hq_vl *
38:	em_sy *
39:	em_hq_jun *
40:	em_hq_mus *
41:	em_hq_other *

Pred. No. is the number of results predicted by chance to have a

Symbol	Definition	Units
\mathcal{A}	Amplitude	cm
\mathcal{B}	Broadening	cm
\mathcal{C}	Concentration	g/g
\mathcal{D}	Diffusion coefficient	cm ² /s
\mathcal{E}	Energy	J
\mathcal{F}	Force	N
\mathcal{G}	Gravitational constant	m ³ /kg s ²
\mathcal{H}	Heat	J
\mathcal{I}	Intensity	W/m ²
\mathcal{J}	Current density	A/m ²
\mathcal{K}	Permeability	W/m K
\mathcal{L}	Length	cm
\mathcal{M}	Mass	kg
\mathcal{N}	Number of particles	-
\mathcal{O}	Optical density	-
\mathcal{P}	Pressure	N/m ²
\mathcal{Q}	Heat flux	W/m ²
\mathcal{R}	Resistance	Ω
\mathcal{S}	Surface area	m ²
\mathcal{T}	Temperature	K
\mathcal{U}	Velocity	m/s
\mathcal{V}	Volume	m ³
\mathcal{W}	Work	J
\mathcal{X}	Conductivity	W/m K
\mathcal{Y}	Yield stress	N/m ²
\mathcal{Z}	Impedance	Ω
\mathcal{a}	Acceleration	m/s ²
\mathcal{b}	Broadening	cm
\mathcal{c}	Concentration	g/g
\mathcal{d}	Diffusion coefficient	cm ² /s
\mathcal{e}	Energy	J
\mathcal{f}	Force	N
\mathcal{g}	Gravitational constant	m ³ /kg s ²
\mathcal{h}	Heat	J
\mathcal{i}	Intensity	W/m ²
\mathcal{j}	Current density	A/m ²
\mathcal{k}	Permeability	W/m K
\mathcal{l}	Length	cm
\mathcal{m}	Mass	kg
\mathcal{n}	Number of particles	-
\mathcal{o}	Optical density	-
\mathcal{p}	Pressure	N/m ²
\mathcal{q}	Heat flux	W/m ²
\mathcal{r}	Resistance	Ω
\mathcal{s}	Surface area	m ²
\mathcal{t}	Temperature	K
\mathcal{u}	Velocity	m/s
\mathcal{v}	Volume	m ³
\mathcal{w}	Work	J
\mathcal{x}	Conductivity	W/m K
\mathcal{y}	Yield stress	N/m ²
\mathcal{z}	Impedance	Ω

2000

Result	No.	Score	Match	Country	1st	2nd	3rd	4th	5th	6th	7th	8th	9th	10th	11th	12th	13th	14th	15th	16th	17th	18th	19th	20th	21st	22nd	23rd	24th	25th	26th	27th	28th	29th	30th	31st	32nd	33rd	34th	35th	36th	37th	38th	39th	40th	41st	42nd	43rd	44th	45th	46th	47th	48th	49th	50th	51st	52nd	53rd	54th	55th	56th	57th	58th	59th	60th	61st	62nd	63rd	64th	65th	66th	67th	68th	69th	70th	71st	72nd	73rd	74th	75th	76th	77th	78th	79th	80th	81st	82nd	83rd	84th	85th	86th	87th	88th	89th	90th	91st	92nd	93rd	94th	95th	96th	97th	98th	99th	100th	101st	102nd	103rd	104th	105th	106th	107th	108th	109th	110th	111th	112th	113th	114th	115th	116th	117th	118th	119th	120th	121st	122nd	123rd	124th	125th	126th	127th	128th	129th	130th	131st	132nd	133rd	134th	135th	136th	137th	138th	139th	140th	141st	142nd	143rd	144th	145th	146th	147th	148th	149th	150th	151st	152nd	153rd	154th	155th	156th	157th	158th	159th	160th	161st	162nd	163rd	164th	165th	166th	167th	168th	169th	170th	171st	172nd	173rd	174th	175th	176th	177th	178th	179th	180th	181st	182nd	183rd	184th	185th	186th	187th	188th	189th	190th	191st	192nd	193rd	194th	195th	196th	197th	198th	199th	200th	201st	202nd	203rd	204th	205th	206th	207th	208th	209th	210th	211st	212nd	213rd	214th	215th	216th	217th	218th	219th	220th	221st	222nd	223rd	224th	225th	226th	227th	228th	229th	230th	231st	232nd	233rd	234th	235th	236th	237th	238th	239th	240th	241st	242nd	243rd	244th	245th	246th	247th	248th	249th	250th	251st	252nd	253rd	254th	255th	256th	257th	258th	259th	260th	261st	262nd	263rd	264th	265th	266th	267th	268th	269th	270th	271st	272nd	273rd	274th	275th	276th	277th	278th	279th	280th	281st	282nd	283rd	284th	285th	286th	287th	288th	289th	290th	291st	292nd	293rd	294th	295th	296th	297th	298th	299th	300th	301st	302nd	303rd	304th	305th	306th	307th	308th	309th	310th	311st	312nd	313rd	314th	315th	316th	317th	318th	319th	320th	321st	322nd	323rd	324th	325th	326th	327th	328th	329th	330th	331st	332nd	333rd	334th	335th	336th	337th	338th	339th	340th	341st	342nd	343rd	344th	345th	346th	347th	348th	349th	350th	351st	352nd	353rd	354th	355th	356th	357th	358th	359th	360th	361st	362nd	363rd	364th	365th	366th	367th	368th	369th	370th	371st	372nd	373rd	374th	375th	376th	377th	378th	379th	380th	381st	382nd	383rd	384th	385th	386th	387th	388th	389th	390th	391st	392nd	393rd	394th	395th	396th	397th	398th	399th	400th	401st	402nd	403rd	404th	405th	406th	407th	408th	409th	410th	411st	412nd	413rd	414th	415th	416th	417th	418th	419th	420th	421st	422nd	423rd	424th	425th	426th	427th	428th	429th	430th	431st	432nd	433rd	434th	435th	436th	437th	438th	439th	440th	441st	442nd	443rd	444th	445th	446th	447th	448th	449th	450th	451st	452nd	453rd	454th	455th	456th	457th	458th	459th	460th	461st	462nd	463
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ANNALS

[illegible]

[illegible][illegible]

DEFINITION

Homo sapiens (Homo sapiens) is a species of the genus Homo, which is a member of the family Hominidae. It is the only extant member of the subgenus Homo.

ABBREVIATION

ATC10000

KEYWORDS

Homo sapiens

REFERENCES

1. (Class 1 to 1, 2, 3)
Homo sapiens (Homo sapiens) is a species of the genus Homo, which is a member of the family Hominidae. It is the only extant member of the subgenus Homo.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 19:05:18, Search time 749.185 seconds

(without alignments)
1419 743 million cell updates/sec

Title: US-10-009-962-4

Perfect score: 26

Sequence: 1 GGTTCGAACTGCTAGCTGCAATTAATG 26

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 288871 seqs, 20154812384 residues

Total number of hits satisfying chosen parameters: 5777122

Minimum BL seq length: 0

Maximum BL seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database: GenEmbl
1: gb_fa:
2: gb_hg:
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6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
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28: em_un:
29: em_vl:
30: em_hg_hum:
31: em_hg_in:
32: em_hg_other:
33: em_hg_mus:
34: em_hg_plu:
35: em_hg_rca:
36: em_hg_mam:
37: em_hg_vrl:
38: em_sy:
39: em_hg_hum:
40: em_hg_mus:
41: em_hg_other:
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Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being listed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Quality Match Length (bp)	ID	Accession	Source
1	19.6	75.4	127954	2	AC022835
2	19.6	75.4	127954	2	AC022835
3	18.6	71.5	84705	2	AC012573
4	18.6	71.5	80247	2	AC012573
5	18.6	71.5	92942	9	BS0753010
6	18.6	71.5	130462	3	U376617
7	18.6	71.5	152197	2	AC011154
8	18.6	71.5	162234	2	AC007563
9	18.6	71.5	163229	9	AC115085
10	18.6	71.5	172224	2	AC115085
11	18.6	71.5	176097	2	AC115085
12	18.6	71.5	238797	2	AC110480
13	18.6	71.5	263442	2	AC119401
14	18.2	70.0	46924	4	PM163002
15	18.2	70.0	91187	9	AC024790
16	18.2	70.0	151132	2	AC114368
17	18.2	70.0	202928	10	AC115147
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ALL INFORMATION

Result No.	Score	Quality Match Length (bp)	ID	Accession	Source
1	19.6	75.4	127954	2	AC022835
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5	18.6	71.5	92942	9	BS0753010
6	18.6	71.5	130462	3	U376617
7	18.6	71.5	152197	2	AC011154
8	18.6	71.5	162234	2	AC007563
9	18.6	71.5	163229	9	AC115085
10	18.6	71.5	172224	2	AC115085
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12	18.6	71.5	238797	2	AC110480
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TITLE
JOURNAL

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Phonphong, P., Piro, R., Raymond, C., Ruff, L., Siro, C., Siro, P.,
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Smith, C., Spencer, B., Stange, Thomas, N., Stojanovic, N., Talamas, J.,
Tessier, S., Theodor, T., Tefke, K., Tetterton, M., Vassiliev, H.,
Viel, P., Vo, A., Wilson, R., Wu, X., Wyman, P., Young, G., Zaitoun, J.,
Zelick, T., Zimmer, A., and Zody, M.
Direct Submission
Submitted (30 SEP 2002) Whitehead Institute MIT Center for Genome Research
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 5, 2002 this sequence submission replaced a previous one.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.cse.washington.edu/bioinformatics/RepeatMasker/>

Genome Center

Center: Whitehead Institute, MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L2917
Center clone name: 6_P25

Summary Statistics

Sequencing vector: M13, M7815, 4% of reads
Sequencing vector: Phasmid, 57% of reads
Chemistry: Dye termination Eht Eye, 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 151639 bases at least 200
Consensus quality: 152560 bases at least 220
Consensus quality: 152571 bases at least 220
Insert size: 16000; average=16
Insert size: 15277; sum of reads
Quality coverage: 161 in 920 bases; average=16
Quality coverage: 16.1 in 920 bases

* NOTE: This is a working draft sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 16710: contig of 16710 bp in length
* 16711 16710: gap of 100 bp
* 16811 20375: contig of 2555 bp in length
* 20376 20475: gap of 100 bp
* 20476 40955: contig of 20299 bp in length
* 40956 40956: gap of 100 bp
* 40956 100366: contig of 59411 bp in length
* 100367 100466: gap of 100 bp
* 100467 153187: contig of 52721 bp in length
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FEATURES

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/note="assembly_fragment"

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COMMENT: On T-1, 2000 + his separate residence for 2001.

Genome Center		Sequencing Center	
Center: Washington University Genome Sequencing Center			
Center web: WGCSC			
Web site: http://genome.wustl.edu/genome/seq/			
Project Information			
Center project name: H_MH0205012			
Summary Statistics			
Sequencing vector: M13, 73%			
Sequencing method: plus-minus, 97%			
Chemistry: Dye-terminator ET, 73% of reads			
Chemistry: Dye-terminator ET, 27% of reads			
Assembly program: Phrap, version 0.990016			
Consensus quality: 167798 bases at least Q40			
Consensus quality: 171101 bases at least Q30			
Consensus quality: 172282 bases at least Q20			
Insert size: 187000; average=17			
Insert size: 176197; sum-of-coverage			
Quality coverage: 2.54 in Q20 bases, 143600 bp			
Quality coverage: 4.10 in Q20 bases, 340000 bp			
<p>NOTE: This is a working draft sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence, as soon as it is available and the accession number will be preserved.</p>			
1	1477: contig of 1477 bp in length		
1478	1577: gap of unknown length		
1578	3566: contig of 1989 bp in length		
3567	3666: gap of unknown length		
3667	5440: contig of 1774 bp in length		
5441	5540: gap of unknown length		
5541	8092: contig of 3552 bp in length		
8093	8192: gap of unknown length		
8193	10790: contig of 2607 bp in length		
10800	10890: gap of unknown length		
10900	16410: contig of 5511 bp in length		
16411	16510: gap of unknown length		
16511	21762: contig of 5252 bp in length		
21763	21863: gap of unknown length		
21863	27029: contig of 5014 bp in length		
27029	27129: gap of unknown length		
27129	33120: contig of 5042 bp in length		
33121	33220: gap of unknown length		
33121	33221: contig of 2252 bp in length		
33221	39572: gap of unknown length		
39473	39572: gap of unknown length		
39573	48260: contig of 3689 bp in length		
48261	48360: gap of unknown length		
48361	56755: contig of 8355 bp in length		
56757	56856: gap of unknown length		
56857	65334: contig of 2728 bp in length		
65335	65434: gap of unknown length		
65435	75570: contig of 10236 bp in length		
75571	75770: gap of unknown length		
75771	87026: contig of 11256 bp in length		
87027	87126: gap of unknown length		
87127	95477: contig of 12951 bp in length		
95478	95577: gap of unknown length		
95578	111227: contig of 11550 bp in length		

[illegible]

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XX 10-AUG-2001: 2001W0-US24129.
 PF XX
 PK 11-AUG-2000: 2000US 224929P.
 XX XX
 PA (WISC) WISC NOUN ALUMNI REG F-IND.
 XX XX
 P1 Triplet FW, Herlache TG;
 XX XX
 DR WP1: 2002-259144/31.
 DR P-15DR: AAE22534, AAE22544, AAE22545, AAE22546, AAE22547, AAE22548,
 DR AAE22539.
 XX XX
 PT Controlling crown gall disease on plants comprises: transfecting the
 PT plant with a biologically pure culture of an alpha-proteobacterial
 PT strain which produces tritoliotoxin of which is engineered to produce
 PT tritoliotoxin .
 XX XX
 PS Claim 6: Page 23-32; 46pp; English.
 XX XX
 CC The invention relates to a method for controlling crown gall disease in
 CC plants using an effective quantity of alpha proteobacteria strain that
 CC produces tritoliotoxin (tlk) or engineered to produce tritoliotoxin. The
 CC invention also provides a biocontrol agent for use in the method, and
 CC a plant coated with the biocontrol control agent. The method is useful
 CC for controlling crown gall disease. The alpha-proteobacteria strain
 CC that produces tritoliotoxin is useful as a biocontrol agent for crown
 CC gall disease in plants. The present sequence is ribosomal beta-mesosome
 CC by tritoliotoxin operon.
 XX XX
 SO Sequence 7142 BP: 1574 A: 1892 C: 1945 G: 1741 T: 0 other:
 Query Match 70.0%; Score 19.6; LR 24; Length 7142
 Best Local Similarity 84.6%; Prot. No. 60;
 Matches 22; Conserved 0; Mismatches 4; Indels 0; Gaps 0
 XX XX
 CY 3 CTGAGAGAGCTGCTTAAGATGAGAG 28
 ID 111111111111111111111111
 ID 49 CTCTAAAGAGCTGCTTAAGATGAG 24
 XX XX
 RESULT 6
 AAA28291
 ID AAA28291 standard: DNA: 40 BP.
 XX XX
 AC AAA28291:
 XX XX
 DT 12-FEB-2001 (first entry)
 XX XX
 DE Human immunoglobulin G1 Fc region gene specific PCR primer SEQ ID 21.
 XX XX
 KW beta-secretase; amyloid plaques; Alzheimer's disease; human
 KW beta's syndrome; amyloid angiopathy; amyloid-beta; amyloid-beta
 KW PCR primer; immunoglobulin G1; IgG1; Fc region; SS.
 XX XX
 OS Homo sapiens.
 XX XX
 IN W0200058479 A1
 XX XX
 PD 05-06-2000
 XX XX
 PE 23-MAR-2000: 2000W0-US07755.
 XX XX
 PK 26-MAR-1999: 9908-0277225.
 XX XX
 PA (AMC-) AMGEN INC.
 XX XX
 P1 Clinton M. Vassar RJ, Bennett MD;
 XX XX
 DR WP1: 2000 594543/56.
 XX XX
 PT Isolated beta-secretase nucleic acids and encoded polypeptides, useful
 PT for diagnosis and gene therapy of Alzheimer's disease .

XX Example 9: Page 10; 14pp; English.
 PS XX
 CC This invention relates to a method for producing effective polypeptides
 CC proteins, beta-secretase, and amyloid plaques, and Alzheimer's disease
 CC of the compound's family of the protein encoded by the gene
 CC invention includes an expression vector, a construct, the polypeptide
 CC sequence, a host cell, and a method for expressing the polypeptide
 CC product. The polypeptide is a beta-secretase, and the polypeptide
 CC included in the invention is a polypeptide, a polypeptide, a polypeptide
 CC beta secretase, a polypeptide, a polypeptide, a polypeptide, a polypeptide
 CC to a beta-secretase, and a polypeptide, a polypeptide, a polypeptide, a polypeptide
 CC levels of beta-secretase, polypeptide, a polypeptide, a polypeptide, a polypeptide
 CC The polypeptide sequence, beta-secretase, exhibits a polypeptide, a polypeptide
 CC nucleotide sequence, the beta-secretase, and a polypeptide, a polypeptide, a polypeptide
 CC map to a region of the beta-secretase, and a polypeptide, a polypeptide, a polypeptide
 CC and as hybridization probes, the polypeptide, a polypeptide, a polypeptide, a polypeptide
 CC of beta-secretase (NA-1) RNA, and as in Alzheimer's disease, a polypeptide, a polypeptide
 CC syndrome, and amyloid angiopathy. The nucleotide sequence, a polypeptide, a polypeptide
 CC used as anti-sense inhibitors of beta-secretase expression, in the
 CC therapy of Alzheimer's disease, and for the identification of a polypeptide, a polypeptide
 CC that modulate beta-secretase activity, and a polypeptide, a polypeptide, a polypeptide
 CC protein may be used for the identification of a polypeptide, a polypeptide, a polypeptide
 CC detect the presence of beta-secretase polypeptide in a sample, a polypeptide, a polypeptide
 CC sample. The present sequence represents a polypeptide, a polypeptide, a polypeptide
 CC DNA encoding the polypeptide of the human immunoglobulin G1 Fc region
 CC In the production of a polypeptide, a polypeptide, a polypeptide, a polypeptide, a polypeptide
 XX XX
 SO Sequence 4 BP: 1574 A: 1892 C: 1945 G: 1741 T: 0 other:
 Query Match 70.0%; Score 19.6; LR 24; Length 7142
 Best Local Similarity 84.6%; Prot. No. 60;
 Matches 22; Conserved 0; Mismatches 4; Indels 0; Gaps 0
 XX XX
 CY 3 CTGAGAGAGCTGCTTAAGATGAGAG 28
 ID 111111111111111111111111
 ID 49 CTCTAAAGAGCTGCTTAAGATGAG 24
 XX XX
 RESULT 7
 AB115957
 ID AB115957 standard: DNA: 40 BP.
 XX XX
 AC AB115957:
 XX XX
 D1 26-MAR-2002 (first entry)
 XX XX
 DE Drosophila melanogaster expressed polypeptide SEQ ID 21.
 XX XX
 KW Drosophila melanogaster; expressed polypeptide; polypeptide; polypeptide
 KW Pharmacological; beta-secretase
 XX XX
 OS Drosophila melanogaster
 XX XX
 IN W0200271042 A1
 XX XX
 PD 27-SEP-2001
 XX XX
 PE 23-MAR-2001: 2001W0-US07755.
 XX XX
 PK 23-MAR-2000: 2000W0-US07755.
 XX XX
 PA (PHE) 13-SEP-2001
 XX XX
 P1 Venturi M, Adams R, Li W, Zhou S, Wu
 XX XX
 DR WP1: 2001 650000/77.
 DR P-15DR: AAE22534, AAE22544, AAE22545, AAE22546, AAE22547, AAE22548,
 DR AAE22539.
 XX XX
 PT New method for producing effective polypeptides, and a polypeptide, a polypeptide, a polypeptide
 PT genes from Drosophila and for identification of polypeptide, a polypeptide, a polypeptide
 PT interactions

11. "Development of a new method for the determination of the
 12. and production plants and animals and the use of the
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member of oligonucleotides and/or peptide nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNPs); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Apol310-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.

2021-10-26 10:52 EDT, 2022-A, 7:07, 144 (5) 1441: 1111002

[illegible]

Best Local Similarity 84.08; Pred. No. 1,400.02;
 Matched 21; Conservative 6; Mismatches 4

Matches: 21; Conservations: 6; Mismatches: 4; Indels: 0; Gaps: 0;

CTGAGAGGTTCTGTAAGGTTCTGAGG 27

[illegible]

420 CTGGATAAACTTGTTAACGTTCTCCG 444

Search completed: August, 14, 2003, 05:52:14
Job time : 184.491 secs

Total time : 184.491 secs



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 97 000 1999 9008 141-188
 98 000 1999 9008 141-189
 99 000 1999 9008 141-190
 100 000 1999 9008 141-191

```

XX
XX 10-AUG-2001: 2001MO-US25120.
XX
XX 11-AUG-2000: 2000US-2244291.
XX
XX (WIS7) WISCONSIN ALUMNI RES FOUND.
XX
XX Triplet BW, Herlache TC;
XX
XX WPT: 2002-269144/31.
XX P-PS08: AAE22533, AAE22534, AAE22535, AAE22536, AAE22537, AAE22538,
XX AAE22539.
XX
XX Controlling crown gall disease on plants comprises transfecting the
XX plant with a biologically pure culture of an alpha-proteobacteria
XX strain which produces tritolicoxin or which is engineered to produce
XX tritolicoxin.
XX
XX Claim 6: Page 23-32: 4pp; English.
XX
XX The invention relates to a method for controlling crown gall disease in
XX plants using an effective quantity of alpha-proteobacteria strain that
XX produces tritolicoxin (Tlx) or engineered to produce tritolicoxin. The
XX invention also provides a biocontrol agent for use in the method, and
XX a plant coated with the biological control agent. The method is useful
XX for controlling crown gall disease. The alpha-proteobacteria strain
XX that produces tritolicoxin is useful as a biocontrol agent for crown
XX gall disease in plants. The present sequence is ribosomal protein-18
XX or tritolicoxin Tlx operon.
XX
XX Sequence 7142 BP: 1574 A; 1892 G; 1945 G; 1741 T; 1 other:
XX
XX Query Match Best Local Similarity 70.0%; Score 19.6; DR 24; Length 7142;
XX
XX Matches 22; Conserved: 0; Mismatch: 4; Indel: 0; Gap: 0
XX
XX 1. CGGTCAGCTTAAGAAATTCCTCAG 26
XX 111111111111111111111111
XX 24 TGGTAAACCAATAAATAAGTTTAAAG 49
XX
XX
XX RESULT 6
XX ID AAA28291 standard, BNA, 49 BP.
XX
XX AA28291:
XX
XX 12-PEB-2001 (first entry)
XX
XX Human immunoglobulin G1 Fc region gene specific PCR primer SEQ ID 21.
XX
XX beta-secretase; amyloid plaque; Alzheimer's disease; human;
XX Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective;
XX PCR primer; immunoglobulin G1; IgG1, Fc region; ss.
XX
XX Homo sapiens.
XX
XX W2000058479-A1.
XX
XX 05-0CT-2000.
XX
XX 23-MAR-2000: 2000MO-US07755.
XX
XX 26-MAR-1999: 9908-0277229.
XX
XX (AMOE) AMCHN INC.
XX
XX CITRUS M. VASSAR RJ, BENNETT BD;
XX
XX WPT: 2000-594643/56.
XX
XX Isolated beta-secretase nucleic acids and encoded polypeptides, used
XX for diagnosis and gene therapy of Alzheimer's disease.

```

```

XX
XX Exam to 9: 140: 100: 100: 100: 100:
XX
XX This invention relates to a method for controlling crown gall disease in
XX plants using an effective quantity of alpha-proteobacteria strain that
XX produces tritolicoxin (Tlx) or engineered to produce tritolicoxin. The
XX invention also provides a biocontrol agent for use in the method, and
XX a plant coated with the biological control agent. The method is useful
XX for controlling crown gall disease. The alpha-proteobacteria strain
XX that produces tritolicoxin is useful as a biocontrol agent for crown
XX gall disease in plants. The present sequence is ribosomal protein-18
XX or tritolicoxin Tlx operon.
XX
XX Sequence 7142 BP: 1574 A; 1892 G; 1945 G; 1741 T; 1 other:
XX
XX Query Match Best Local Similarity 70.0%; Score 19.6; DR 24; Length 7142;
XX
XX Matches 22; Conserved: 0; Mismatch: 4; Indel: 0; Gap: 0
XX
XX 1. CGGTCAGCTTAAGAAATTCCTCAG 26
XX 111111111111111111111111
XX 24 TGGTAAACCAATAAATAAGTTTAAAG 49
XX
XX
XX RESULT 7
XX ID ABL100572 standard, cDNA, 49 BP.
XX
XX ABL100572:
XX
XX 26-MAR-1992 (first entry)
XX
XX Human immunoglobulin G1 Fc region gene specific PCR primer SEQ ID 21.
XX
XX beta-secretase; amyloid plaque; Alzheimer's disease; human;
XX Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective;
XX PCR primer; immunoglobulin G1; IgG1, Fc region; ss.
XX
XX Homo sapiens.
XX
XX W2000058479-A1.
XX
XX 05-0CT-2000.
XX
XX 23-MAR-2000: 2000MO-US07755.
XX
XX 26-MAR-1999: 9908-0277229.
XX
XX (AMOE) AMCHN INC.
XX
XX CITRUS M. VASSAR RJ, BENNETT BD;
XX
XX WPT: 2000-594643/56.
XX
XX P-PS08: AAB69841.
XX
XX Now isolated nucleic acids and encoded polypeptides, used for
XX diagnosis and gene therapy of Alzheimer's disease.
XX
XX

```


XX therapy. It can also be used to repopulate blood cells in a murine.
 XX The products can also be used to treat, e.g., leukostatic disorders,
 XX arteriosclerosis, type II diabetes, polypoid intestinal diseases,
 XX cardiovascular diseases, osteoarthritis, dermatological disorders,
 XX hypertension, insulin resistance, hypotestosteronemia,
 XX hypotriglyceridemia, cancer and cholestasis.
 XX
 XX Sequence 7127 BP: 1663 A; 1941 G; 1859 G; 1454 T; ...
 Query Match: 68.6%; Score 19.2; 146 BP; Length 7127;
 Best local similarity: 87.5%; Prod. No. 91;
 Matches: 21; Conservation: 91; Mismatches: 0; ...
 4 GTGACCTTACAGCTTCTCTAG 26
 ||||| ||||| ||||| |||||
 2128 GTGACCTTACAGAGCTTCTAG 2151

RESULT 10
 AAT75093
 ID AAT75093 standard: (NA: 7127 BP).
 XX
 AC AAT75093;
 XX
 DI 07-02-1997 (first entry)
 XX
 XX Human obesity protein-human 19c1 CH2CH3 gene fusion.
 DE
 KW Obesity protein, Ob protein, 19c1, hOb, hOb, hOb, hOb, hOb,
 KW weight loss; appetite loss; anorexia; emphysema; hypotestosteronemia;
 XX
 XX Chimera Homo sapiens;
 OS Chimera bacteriophage Sp6;
 OS Chimera SV40 virus;
 OS Chimera herpes simplex virus;
 OS Chimera bacteriophage M13.
 XX
 XX Key Location/Qualifiers
 FH 612
 F1 misc_RNA
 F1 /ftag= a
 F1 /note= "RNA start"
 F1 776..844
 F1 promoter
 F1 /ftag= b
 F1 /note= "Sp6 promoter"
 F1 845
 F1 misc_RNA
 F1 /ftag= c
 F1 /note= "Sp6 RNA start"
 F1 918..2112
 F1 CDS
 F1 /ftag= d
 F1 /1dco1= 08-1901 chimera
 F1 2183
 F1 polyA_signal
 F1 /ftag= e
 F1 /note= "SV40 early polyA"
 F1 2124
 F1 misc_RNA
 F1 /ftag= f
 F1 /note= "SV40 origin"
 F1 2748
 F1 misc_RNA
 F1 /ftag= g
 F1 /note= "pUC118 start"
 F1 2756..2891
 F1 promoter
 F1 /ftag= h
 F1 /note= "TK promoter"
 F1 2892..3892
 F1 CDS
 F1 /ftag= i
 F1 /note= "TK neomycin phosphotransferase gene"
 F1 3893
 F1 terminator
 F1 /ftag= j
 F1 /note= "SV40 L terminator"
 F1 4526..4643
 F1 misc_RNA
 F1 /ftag= k
 F1 /note= "pBR322 sequence"
 F1 4645
 F1 misc_RNA
 F1 /ftag= l
 F1

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 F2 W 97.2444 A1
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 F3 10-01-1997
 XX
 F4 19-02-1997
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 F96 27-04-1997
 XX
 F97 27-04-1997
 XX
 F98 27-04-1997
 XX
 F99 27-04-1997
 XX
 F100 27-04-1997
 XX

22. methoxy, or oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
23. and the degree of hybridisation to both classes is determined from the
24. label on the amplicon. From the ratio of labels hybridised to the two
25. classes of oligomers, the degree of methylation is calculated. The method
26. is used: (i) for diagnosis and/or prognosis of sub-classes of
27. therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
28. of the central nervous, cardiovascular, gastrointestinal and respiratory
29. systems etc., particularly by detecting mutations of single nucleotide
30. polymorphisms (SNPs); and (ii) for differentiation of cell or tissue
31. types and for investigating cell differentiation. The method allows the
32. methylation status of many C residues to be determined simultaneously.
33. A011410-AB054121 represent genomic DNA sequences used to illustrate the
34. method for determining the degree of cytosine methylation described in
35. the disclosure of the invention.

Seq. Sequence 1052 BP; 392 A; 373 C; 143 G; 144 T; 0 other;

Query Match	Score	IR	Length
66.48;	18.6;	24;	1052;
94.09;	14.03;	14;	1052;

Matches: 21; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

2 GTTGGAGCTTAAGGAGCTTCTCGAG 26

414 GGGGAGGTTAAGAGCTTAACGAG 420

Search completed: August 14, 2008, 03:52:15
Job time : 177.491 secs

CC diagnose the presence of *E. faecalis* in a sample of determined the
 CC presence of a specific microbe in a sample. The invention is also useful
 CC for mediating the growth of pathogenicity of *E. faecalis* in a vaccine
 CC to confer resistance to Enterococcal infection for commercial
 CC therapeutic and industrial purposes, and for fermenting a particular
 CC sugar source or to produce a particular metabolite. The invention is
 CC useful for detecting diseases related to Enterococcus infection in
 CC animals, and for detecting *E. faecalis* using a kit provided by the
 CC present nucleic acid sequence represents an Enterococcus *faecalis* coding
 CC DNA sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification but was obtained in electronic format directly
 CC from USPTO at <http://seqdata.uspto.gov>.
 XX
 SO Sequence 7993 BP: 2226 A; 1725 C; 1128 G; 461 T; 4 other:
 Query Match 68.5%; Score 17.8; H: 24; Length 7993
 Host Local Similarity 90.5%; Prod. No. 1.1e+02
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 4 ATTATACGACTAGCACTTGA 23
 ID 11111111111111111111
 DB 6034 ATTATACGACTAGCACTTGA 6054

RESULT 4
 ABX22745
 ID ABX22745 standard: cDNA: 473 BP
 AC ABX22745
 XX
 D1 10-FEB-2003 (first entry)
 XX
 DE Human GTP-mannose 4,6-dehydratase (GM4,6D) [Ena:af022]
 XX
 KW Human GTP-mannose 4,6-dehydratase, GM4,6D, gene, cDNA, full length, full
 KW cDNA, full length, cDNA, full length, cDNA, full length, cDNA, full length,
 KW arthritis, asthma, sepsis, reperfusion injury, stroke, infection,
 KW complex carbohydrate, gene replacement therapy, immunosuppression,
 KW anti-inflammatory, antiarthritic, antibacterial, neuroprotective,
 KW anti-inflammatory, vasodilator,
 XX
 OS Homo sapiens
 XX
 PN US2002110548-A1
 XX
 PD 15-AUG-2002
 XX
 FI 11 JUN 2001, 200103-0879574
 XX
 PR 22-NOV-1996; 9608-0753233
 PR 01-OCT-1997; 9708-0984246
 PR 09-SEP-1998; 9808-0145674
 PR 14-JUN-1999; 9908-0333177
 XX
 PA (GENE) GENETICS INST INC
 PI Sullivan F, Fild P, Fured P
 XX
 DR WPI: 2003-066673/06

CC New composition comprising GTP mannose 4,6 dehydratase (GM4,6D)
 CC peptide, for manufacturing complex carbohydrates, or as targets for
 CC screening GM4,6D antagonists for treating e.g. arthritis, or transplant
 CC rejection
 XX
 PS Disclosure, SEQ ID NO 4804: 6pp; English.
 XX
 CC The invention relates to a composition comprising a human GTP-mannose
 CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
 CC GM4,6D inhibitors, GM4,6D inhibitors are useful for reducing inflammation
 CC in a mammalian subject and for treating or ameliorating diseases affected
 CC by the level of cellular fucosylation or disease affected by the

CC fucosylation of a protein, e.g. those diseases involving arthritis,
 CC transplant rejection, asthma, sepsis, reperfusion injury, stroke,
 CC infection, the GM4,6D peptide or a fragment thereof is useful for
 CC used for manufacturing complex carbohydrates and for fermenting a
 CC particular small molecule and analysis of the activity of the enzyme
 CC polypeptide is used to develop an assay for the presence of the
 CC enzyme, as well as to monitor and control the presence of the
 CC GM4,6D polypeptide and GM4,6D polypeptide expression in a cell or
 CC human GM4,6D polypeptide of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification but was obtained in electronic format directly
 CC at seqdata.uspto.gov/Sequence.html.
 XX
 SO Sequence 473 BP: 201 A; 161 C; 112 G; 461 T; 4 other:
 Query Match 65.7%; Score 17.4; H: 24; Length 473
 Host Local Similarity 85.8%; Prod. No. 872
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 1 GATTAATGATGATGATGATGATGAT 24
 ID 11111111111111111111
 DB 1 GATTAATGATGATGATGATGATGAT 24

RESULT 4
 ABQ70746
 ID ABQ70746 standard: cDNA: 473 BP
 AC ABQ70746
 XX
 D1 07-OCT-2002 (first entry)
 XX
 DE Human GTP-mannose 4,6-dehydratase (GM4,6D) [Ena:af022]
 XX
 KW Human GTP-mannose 4,6-dehydratase, GM4,6D, gene, cDNA, full length, full
 KW cDNA, full length, cDNA, full length, cDNA, full length, cDNA, full length,
 KW arthritis, asthma, sepsis, reperfusion injury, stroke, infection,
 KW complex carbohydrate, gene replacement therapy, immunosuppression,
 KW anti-inflammatory, antiarthritic, antibacterial, neuroprotective,
 KW anti-inflammatory, vasodilator,
 XX
 OS Homo sapiens
 XX
 PN W: 2002110548-A1
 XX
 PD 20 JUN 2002
 XX
 FI 01 OCT 2001; 200103-0879574
 XX
 PR 41 OCT 2000; 200008-2447474
 XX
 PA (GENE) GENETICS INST
 PI Sun Y, Koopman H, Fild P, Fured P
 XX
 DR WPI: 2002-066673/06

CC New composition comprising GTP mannose 4,6 dehydratase (GM4,6D)
 CC peptide, for manufacturing complex carbohydrates, or as targets for
 CC screening GM4,6D antagonists for treating e.g. arthritis, or transplant
 CC rejection
 XX
 PS Disclosure, SEQ ID NO 4804: 6pp; English.
 XX
 CC The invention relates to a composition comprising a human GTP-mannose
 CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
 CC GM4,6D inhibitors, GM4,6D inhibitors are useful for reducing inflammation
 CC in a mammalian subject and for treating or ameliorating diseases affected
 CC by the level of cellular fucosylation or disease affected by the
 CC cDNA sequences are useful for producing transgenic animals and cells

CC discloses genomic DNA sequences (AB016176-AB016177), expressed RNA
 CC sequences (AB016180-AB016175) and the encoded proteins
 CC (AB016173-AB016172).
 CC The sequence data for this patent did not form part of the prior art
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/pubdata/seq_sequences.
 CC
 XX Sequence 7228 BF: 2135 A, 1417 C, 1507 T, 2125 T, 0 other.
 XX
 XX Query Match 66.2%; Score 17.2; DB 23; Length 7228
 XX Best Local Similarity 85.4%; Prod. No. 26067
 XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0
 XX
 XX 1 GATTATACGCTACCTCG 22
 XX 11111111111111111111
 XX DB 5336 GATTATACGCTACGCTCG 5315
 XX
 XX RESULT 11
 XX AB016096/0
 XX ID AB016096 standard, RNA, 685 bp.
 XX AC AB016096/
 XX XX
 XX 12-JUL-2002 (first entry)
 XX DE oligonucleotide for detecting cytosine methylation SEQ ID NO 2687.
 XX
 XX KW Human: cytosine methylation; 5'-CpG-3'; orally cytotoxic diseases;
 XX drug; side effect; cancer; central nervous system; cardiovascular;
 XX gastrointestinal; respiratory system; single nucleotide polymorphism;
 XX SNP; cell differentiation; ds.
 XX
 XX OS Homo sapiens.
 XX
 XX FN W020218632 A2.
 XX PD 07-MAR-2002.
 XX PF 01-SEP-2001; 2001WC-EP10074.
 XX PR 01-SEP-2003; 2003DE 1049826.
 XX PP 05-SEP-2000; 2000PF-1044543
 XX
 XX PA (EP10-) EP10ENOMICS A1.
 XX
 XX PI Oluk A., Fliegerbrock C., Berlin K., Guedin P.
 XX WPI: 2002-371829/10.
 XX
 XX PI Determining the degree of cytosine methylation in genomic DNA useful
 XX for diagnosis and prognosis, comprises selective hybridization of
 XX amplicons from chemically treated DNA
 XX
 XX Claim 12: 56pp + Sequence Listing: 56pp; German.
 XX
 XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a methyl cytosine present in a
 XX genomic sample of DNA. The sample is treated chemically to convert
 XX cytosine (C) but not methylated C, to uracil, then part of the genomic
 XX DNA that contains the target C is amplified to form a labeled amplicon.
 XX The amplicon is hybridized to two classes, each with at least one
 XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 XX and the degree of hybridization to both classes is determined from the
 XX label on the amplicon. From the ratio of labels hybridized to the two
 XX classes of oligomers, the degree of methylation is calculated. The method
 XX is used: (i) for diagnosis and/or prognosis of side effects of
 XX therapeutic drugs and of a wide range of diseases, e.g., cancer, diseases
 XX of the central nervous system, cardiovascular, gastrointestinal and respiratory
 XX systems etc., particularly by detecting mutations of single nucleotide
 XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 XX types and for investigating cell differentiation. The method allows the
 XX methylation status of many C residues to be determined simultaneously.

CC AB016111-AB016112) improved detection of RNA sequences used in the prior art
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the present invention.
 CC
 XX Sequence 685 BF: 1600 A, 1417 C, 1507 T, 2125 T, 0 other.
 XX
 XX Query Match 66.2%; Score 17.2; DB 23; Length 685
 XX Best Local Similarity 85.4%; Prod. No. 16067
 XX Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0
 XX
 XX 2 GATTATACGCTACCTCG 22
 XX 11111111111111111111
 XX DB 609 GATTATACGCTACGCTCG 595
 XX
 XX RESULT 14
 XX AB016097
 XX ID AB016097 standard, RNA, 685 bp.
 XX AC AB016097/
 XX XX
 XX 12-JUL-2002 (first entry)
 XX DE oligonucleotide for detecting cytosine methylation SEQ ID NO 2687.
 XX
 XX KW Human: cytosine methylation; 5'-CpG-3'; orally cytotoxic diseases;
 XX drug; side effect; cancer; central nervous system; cardiovascular;
 XX gastrointestinal; respiratory system; single nucleotide polymorphism;
 XX SNP; cell differentiation; ds.
 XX
 XX OS Homo sapiens.
 XX
 XX FN W020218632 A2.
 XX PD 07-MAR-2002.
 XX PF 01-SEP-2001; 2001WC-EP10074.
 XX PR 01-SEP-2003; 2003DE 1049826.
 XX PP 05-SEP-2000; 2000PF-1044543
 XX
 XX PA (EP10-) EP10ENOMICS A1.
 XX
 XX PI Oluk A., Fliegerbrock C., Berlin K., Guedin P.
 XX WPI: 2002-371829/10.
 XX
 XX PI Determining the degree of cytosine methylation in genomic DNA useful
 XX for diagnosis and prognosis, comprises selective hybridization of
 XX amplicons from chemically treated DNA
 XX
 XX Claim 12: 56pp + Sequence Listing: 56pp; German.
 XX
 XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a methyl cytosine present in a
 XX genomic sample of DNA. The sample is treated chemically to convert
 XX cytosine (C) but not methylated C, to uracil, then part of the genomic
 XX DNA that contains the target C is amplified to form a labeled amplicon.
 XX The amplicon is hybridized to two classes, each with at least one
 XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 XX and the degree of hybridization to both classes is determined from the
 XX label on the amplicon. From the ratio of labels hybridized to the two
 XX classes of oligomers, the degree of methylation is calculated. The method
 XX is used: (i) for diagnosis and/or prognosis of side effects of
 XX therapeutic drugs and of a wide range of diseases, e.g., cancer, diseases
 XX of the central nervous system, cardiovascular, gastrointestinal and respiratory
 XX systems etc., particularly by detecting mutations of single nucleotide
 XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 XX types and for investigating cell differentiation. The method allows the
 XX methylation status of many C residues to be determined simultaneously.
 XX
 XX AB016101-AB016102) improved detection of RNA sequences used in the prior art
 XX method for determining the degree of cytosine methylation described in
 XX the disclosure of the present invention.

Database version 3.1.1
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OM nucleotide - nucleotide search, using sw model

Run on: August 14, 2003, 02:24:05 : Search time 17.974 seconds
(8190 Million cell updates/sec)

File: US-10-009-962-1

Percent score: 28

Sequence: 1 GATTCGAAAGACGCTTCAAGCTCGAAGG 28

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Search: 22781902 seqs, 1215228056 total hits

Total number of hits satisfying chosen parameters: 45562764

Minimum hit seq length: 6

Maximum hit seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

EST:*

1: em_estba:*
2: em_estbun:*
3: em_estin:*
4: em_estinu:*
5: em_estlov:*
6: em_estplo:*
7: em_estpro:*
8: em_estro:*
9: qb_est1:*
10: qb_est2:*
11: qb_hic1:*
12: qb_hic3:*
13: qb_estc4:*
14: qb_estc5:*
15: em_estlom:*
16: em_estlom:*
17: em_qss_hum:*
18: em_qss_hum:*
19: em_qss_pit:*
20: em_qss_vit:*
21: em_qss_hum:*
22: em_qss_hum:*
23: em_qss_hum:*
24: em_qss_hum:*
25: em_qss_hum:*
26: em_qss_hum:*
27: em_qss_vit:*
28: qb_qss2:*
29: qb_qss2:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being produced, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB	ID	Description
1	21.2	75.7	555	9	AM597491	AM597491 (250225)
2	20.6	73.6	558	14	U0030790	U0030790 (250225)
3	20.6	73.6	558	29	U0030790	U0030790 (250225)
4	20.2	72.1	503	29	U0030790	U0030790 (250225)

5	19.2	70.0	558	14	U0030790	U0030790 (250225)
6	19.2	70.0	558	14	U0030790	U0030790 (250225)
7	19.2	70.0	558	14	U0030790	U0030790 (250225)
8	19.2	70.0	558	14	U0030790	U0030790 (250225)
9	19.2	70.0	558	14	U0030790	U0030790 (250225)
10	19.2	70.0	558	14	U0030790	U0030790 (250225)
11	19.2	70.0	558	14	U0030790	U0030790 (250225)
12	19.2	70.0	558	14	U0030790	U0030790 (250225)
13	19.2	70.0	558	14	U0030790	U0030790 (250225)
14	19.2	70.0	558	14	U0030790	U0030790 (250225)
15	19.2	70.0	558	14	U0030790	U0030790 (250225)
16	19.2	70.0	558	14	U0030790	U0030790 (250225)
17	19.2	70.0	558	14	U0030790	U0030790 (250225)
18	19.2	70.0	558	14	U0030790	U0030790 (250225)
19	19.2	70.0	558	14	U0030790	U0030790 (250225)
20	19.2	70.0	558	14	U0030790	U0030790 (250225)
21	19.2	70.0	558	14	U0030790	U0030790 (250225)
22	19.2	70.0	558	14	U0030790	U0030790 (250225)
23	19.2	70.0	558	14	U0030790	U0030790 (250225)
24	19.2	70.0	558	14	U0030790	U0030790 (250225)
25	19.2	70.0	558	14	U0030790	U0030790 (250225)
26	19.2	70.0	558	14	U0030790	U0030790 (250225)
27	19.2	70.0	558	14	U0030790	U0030790 (250225)
28	19.2	70.0	558	14	U0030790	U0030790 (250225)
29	19.2	70.0	558	14	U0030790	U0030790 (250225)
30	19.2	70.0	558	14	U0030790	U0030790 (250225)
31	19.2	70.0	558	14	U0030790	U0030790 (250225)
32	19.2	70.0	558	14	U0030790	U0030790 (250225)
33	19.2	70.0	558	14	U0030790	U0030790 (250225)
34	19.2	70.0	558	14	U0030790	U0030790 (250225)
35	19.2	70.0	558	14	U0030790	U0030790 (250225)
36	19.2	70.0	558	14	U0030790	U0030790 (250225)
37	19.2	70.0	558	14	U0030790	U0030790 (250225)
38	19.2	70.0	558	14	U0030790	U0030790 (250225)
39	19.2	70.0	558	14	U0030790	U0030790 (250225)
40	19.2	70.0	558	14	U0030790	U0030790 (250225)
41	19.2	70.0	558	14	U0030790	U0030790 (250225)
42	19.2	70.0	558	14	U0030790	U0030790 (250225)
43	19.2	70.0	558	14	U0030790	U0030790 (250225)
44	19.2	70.0	558	14	U0030790	U0030790 (250225)
45	19.2	70.0	558	14	U0030790	U0030790 (250225)

REFERENCES

RESULT 1	AM597491	AM597491 (250225)
LOCUS	U0030790	U0030790 (250225)
DEFINITION	U0030790 (250225)	U0030790 (250225)
ACCESSION	U0030790	U0030790 (250225)
VERSION	U0030790	U0030790 (250225)
KEYWORDS	U0030790	U0030790 (250225)
SOURCE	U0030790	U0030790 (250225)
ORGANISM	U0030790	U0030790 (250225)
REFERENCE	U0030790	U0030790 (250225)
AUTHORS	U0030790	U0030790 (250225)
TITLE	U0030790	U0030790 (250225)
ABSTRACT	U0030790	U0030790 (250225)
COMMENT	U0030790	U0030790 (250225)

BASE COUNT	178 a	137 c	192 g	146 t
ORIGIN	/clone="B01621" /clone.lib="B01621" 2 kb cont /note="Vector: pGEM1, Site 1, pGEM1, 1.6 kb, observed total DNA inserted into pGEM1 using RSTX ligators"			
Query Match	72.6%	Score 20.6	DB 2%	Length 653
Best Local Similarity	86.2%	Prod No. 60		
Matches	23	Conservative	0	Mismatches 4
				Indels 0
				Gaps 0
07	2	CGTCGAGAGGCTCTTAAGTGGC 28		
DB	669	CGTCGAGAGGAGTCAATAGGTGGC 635		
RESULT 4				
LOCUS	CG424864	803 bp	ENA	1997
DEFINITION	POM1670 280,610,000 bp Zea mays genomic clone ZM167020			
ACCESSION	CG424864			
VERSION	CG424864.1	GI:20901954		
KEYWORDS	GS.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Angiosperms, Poales, Poaceae, Zea, clade: Panicoidae, Andropogonoideae, Zea, 1 (bases 1 to 803)			
AUTHORS	Whitelaw, C.A., Zoubak, J., Yu, A., Fraser, W., Yuan, Y., San Miguel, P., Ma, J. and Benfey, J.			
TITLE	Maize Genomics Consortium			
JOURNAL	Unpublished			
COMMENT	Contact: Cathy Whitelaw			
	TIGR			
	4713 Medical Center Drive, Rockville, MD 20850, USA			
	Tel: 301-838-5843			
	Fax: 301-838-0208			
	Email: whitelaw@tigr.org			
	Seq primer: TF			
	Class: Sheared ends.			
FEATURES	Location/Qualifiers			
source	1..803			
	/organism="Zea mays"			
	/mol_type="genomic DNA"			
	/strain="B73"			
	/db_xref="taxon:1572"			
	/clone="ZM167020"			
	/clone.lib="ZM167020"			
	/note="Vector: pGEM1-030, Site 1, pGEM1, 0.6 kb, Rb, high			
	GOT selected genomic DNA library"			
BASE COUNT	244 a	162 c	161 g	256 t
ORIGIN				
Query Match	72.1%	Score 20.2	DB 2%	Length 653
Best Local Similarity	86.0%	Prod No. 10-02		
Matches	22	Conservative	0	Mismatches 2
				Indels 0
				Gaps 0
07	2	CGTCGAGAGGCTCTTAAGTGGC 26		
DB	492	CTTCGAGAGGCTCTTAAGTGGC 516		
RESULT 5				
LOCUS	B0102444	594 bp	mRNA	1997
DEFINITION	1091018F01.x1 1091 - Immature ear with common ESTs screened by			
ACCESSION	B0102444			
VERSION	B0102444.1	GI:22522605		
KEYWORDS	EST.			
SOURCE	Zea mays			

[illegible]

Durham, NC 27708-1003
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu

FEATURES

Source

1. 536

/organism "Chlamydomonas reinhardtii"

/mol_type "mRNA"

/strain "CC 1690 wild type mt-2101"

/db_xref "taxon:3055"

/clone_1lib "CC_reinhardt11 CC-1690", Stress 11 (normalized)

/note "Vector: Phagescript II SK+ (Stratagene)"

/note "Stress condition 11 library constructed by John

Reyes and Jeffrey M. Barette, conditions: 1000 cells grown to mid-log phase in TAP (NH₄ condition)

and shifted to TAP + Me₂SO (24hr), 12 probe from

conditions (0, 12hr, 24hr) see Miller et al (2000) Plant

Phys. 122: 127-135; TAP + H₂O₂ (1, 12, 24 hr); TAP +

sorbitol (1, 2, 5, 24 hr); TAP + NaCl (1, 2, 5, 24 hr).

polyA mRNA was purified from each sample, pooled and cDNA

synthesized. The cDNA was directly cloned into Lambda

zap 1 (clonase) in the EcoRV (5') and XbaI (3')

sites. Phagescript II SK+ phageids were excised from the

lambda Zap clones by superinfection with ExAssist

(Stratagene) phage. The library was normalized using

method 4 described in Renaldi et al. (1996) Genome

Research 6: 791-806."

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Research 6: 791-806."

/organism "mRNA"

/strain "CC 1690 wild type mt-2101"

/db_xref "taxon:3055"

/clone_1lib "CC_reinhardt11 CC-1690", Stress 11 (normalized)

/note "Vector: Phagescript II SK+ (Stratagene)"

/note "Stress condition 11 library constructed by John

Reyes and Jeffrey M. Barette, conditions: 1000 cells grown to mid-log phase in TAP (NH₄ condition)

and shifted to TAP + Me₂SO (24hr), 12 probe from

conditions (0, 12hr, 24hr) see Miller et al (2000) Plant

Phys. 122: 127-135; TAP + H₂O₂ (1, 12, 24 hr); TAP +

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method 4 described in Renaldi et al. (1996) Genome

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4444 Forest Park Atlanta, GA 30350
Tel: 404 296 1200
Fax: 404 296 1801

Email: east@arabidopsis.org

This clone is available through the Arabidopsis Biological Resource Center (ABRC) at the University of Missouri, Columbia, MO. For more information, please contact the ABRC at (660) 543-5500 or visit our website at <http://abrc.missouri.edu>.

Insert length: 1.2 kb
Insert type: cDNA

High quality sequencing: 1470

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Insert length: 1.2 kb
Insert type: cDNA
High quality sequencing: 1470

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 POSITION: POSITION
 ADDRESS: ADDRESS

DATE: DATE
 TIME: TIME
 LOCATION: LOCATION

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Durham, NC 27709 1000
Tel: 919 613 8154
Fax: 919 613 8177
Email: chausser@duke.edu
Local: 100/200/400/1000/10000

FEATURES

Source

/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21hr"
/db_xref="taxon:3055"
/clone_lib="CC-reinhardtii CC-1690. Stress II (normalized)
/lambda Zap II"

Query Match 70.0% Score 19.63 DB 100 Length 5763
Best Local Similarity 84.6% Evid: No. 1.6e-027
Matches 22 Conservative 0 Mismatches 1 Indels 0 Gaps 0
ORIGIN
BASE COUNT 108 a 177 c 149 g 102 t
Research 6: 791-806"

Query Match 70.0% Score 19.63 DB 100 Length 5763
Best Local Similarity 84.6% Evid: No. 1.6e-027
Matches 22 Conservative 0 Mismatches 1 Indels 0 Gaps 0
ORIGIN
BASE COUNT 108 a 177 c 149 g 102 t
Research 6: 791-806"

LOCUS CD259489 549 bp mRNA linear not annotated
DEFINITION F5M093205F125452 SM. Phytophthora sojae grown in synthetic
medium Phytophthora sojae cDNA library SHM001005, 1994 sequenced.
ACCESSION CD259489
VERSION CD259489.1 GI:31047316
KEYWORDS EST
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 549)
Tyler B.M., Jackson, H.S., Gijzen, M., Tsao, E.H., and Woudenberg,
U.S.A.-FRAN: Expression of phytophthora sojae genes during infection
and propagation
Unpublished
Contact: Tyler B
Tyler lab
VBI
180 Pratt Dr., Pleasantburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyl@vt.edu

PCR Primers
FORWARD: BK reverse
Plate: 003 row 1, column 05
Seq primer: BK reverse
High quality sequence stop 540
Location/Qualifiers
1..549
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67594"

FEATURES

Source

/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67594"

Query Match 70.0% Score 19.63 DB 100 Length 5763
Best Local Similarity 84.6% Evid: No. 1.6e-027
Matches 22 Conservative 0 Mismatches 1 Indels 0 Gaps 0
ORIGIN
BASE COUNT 108 a 177 c 149 g 102 t
Research 6: 791-806"

Query Match 70.0% Score 19.63 DB 100 Length 5763
Best Local Similarity 84.6% Evid: No. 1.6e-027
Matches 22 Conservative 0 Mismatches 1 Indels 0 Gaps 0
ORIGIN
BASE COUNT 108 a 177 c 149 g 102 t
Research 6: 791-806"

LOCUS BM135377 5763 bp mRNA linear not annotated
DEFINITION F5M093205F125452 SM. Phytophthora sojae grown in synthetic
medium Phytophthora sojae cDNA library SHM001005, 1994 sequenced.
ACCESSION BM135377
VERSION BM135377.1 GI:31047316
KEYWORDS EST
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 5763)
Tyler B.M., Jackson, H.S., Gijzen, M., Tsao, E.H., and Woudenberg,
U.S.A.-FRAN: Expression of phytophthora sojae genes during infection
and propagation
Unpublished
Contact: Tyler B
Tyler lab
VBI
180 Pratt Dr., Pleasantburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyl@vt.edu

PCR Primers
FORWARD: BK reverse
Plate: 003 row 1, column 05
Seq primer: BK reverse
High quality sequence stop 5763
Location/Qualifiers
1..5763
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67594"

Query Match 70.0% Score 19.63 DB 100 Length 5763
Best Local Similarity 84.6% Evid: No. 1.6e-027
Matches 22 Conservative 0 Mismatches 1 Indels 0 Gaps 0
ORIGIN
BASE COUNT 108 a 177 c 149 g 102 t
Research 6: 791-806"

Query Match 70.0% Score 19.63 DB 100 Length 5763
Best Local Similarity 84.6% Evid: No. 1.6e-027
Matches 22 Conservative 0 Mismatches 1 Indels 0 Gaps 0
ORIGIN
BASE COUNT 108 a 177 c 149 g 102 t
Research 6: 791-806"

Query Match 70.0% Score 19.63 DB 100 Length 5763
Best Local Similarity 84.6% Evid: No. 1.6e-027
Matches 22 Conservative 0 Mismatches 1 Indels 0 Gaps 0
ORIGIN
BASE COUNT 108 a 177 c 149 g 102 t
Research 6: 791-806"

University of Minnesota (Genetic and Biochemistry), St. Paul, MN, U.S.A. (Dr. J. Venter, et al.). The cDNA library should contain genes of both short and long pathogen origin. Plasmid RNA prepared from and RNA preparation were performed in the of Anderson Lab (Cell Culture Methods).

BASE COUNT 155 nt (21 nt of other reference)

GENE NAME 79,000 bp (10,000 bp) (10,000 bp)

GENE LOCUS 79,000 bp (10,000 bp) (10,000 bp)

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GenBank version 5.1.6
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OM nucleotide nucleotide search, using sw model

Run on: August 14, 2003, 02:24:05 (with all parameters)
391,190 Million Cell updates/sec

Title: US-10-009-962-3

Perfect score: 25
Sequence: 1 GCATTAATCACTAATATTGGAAGG 26

Scoring table: Identity_NUC
Gapop 10.0, Gapext 1.0

Search: 2281992 seqs, 1222232056 residues

Total number of hits satisfying chosen parameters: 4552734

Minimum hit seq length: 0
Maximum hit seq length: 200000000

Post-processing: Minimum Match 99
Listing first 45 summaries

Database:

EST:
1: em_estdb:
2: em_esthm:
3: em_estln:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estlv:
8: em_estc:
9: qb_est1:
10: qb_est2:
11: qb_est3:
12: qb_est4:
13: qb_est5:
14: qb_est6:
15: em_esthm:
16: em_estom:
17: em_gss_hum:
18: em_gss_hum:
19: em_gss_pla:
20: em_gss_vit:
21: em_gss_lun:
22: em_gss_mus:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_fod:
26: em_gss_pla:
27: em_gss_vit:
28: qb_gss1:
29: qb_gss2:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result in the printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match length	Hit	Description
1	18.8	72.3	59	A292806.0
2	18.8	72.3	649	B2405494
3	18.8	72.3	680	B2405595
4	18.6	71.7	181	AAT14111

5	18.6	71.5	11	B011002
6	18.6	71.5	11	B011002
7	18.6	71.5	11	B011002
8	18.6	71.5	1007	B011006
9	18.2	70.0	200	B011006
10	18.2	70.0	200	B011006
11	18.2	70.0	200	B011006
12	18.2	70.0	200	B011006
13	18.2	70.0	200	B011006
14	18.2	70.0	200	B011006
15	18.2	70.0	200	B011006
16	18.2	70.0	200	B011006
17	18.2	70.0	200	B011006
18	18.2	70.0	200	B011006
19	18.2	70.0	200	B011006
20	18.2	70.0	200	B011006
21	18.2	70.0	200	B011006
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26	18.2	70.0	200	B011006
27	18.2	70.0	200	B011006
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REFERENCES

RESULT 1
A292806.0
DEFINITION
A292806.0
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
A292806.0
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DEFINITION RNC1 6, 171A1017, RNC1 6 Homo sapiens genomic clone RNC1-6-171A1017, genomic survey sequence.

ACCESSION M0274752

VERSION M0274752.1 GI:1852596

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 391)

AUTHORS Bae, A., Cairo, A., Calabrese, J., Grogawa, K., Van Oost, M., Wu, J. and de Jong, P.J.

TITLE BAC and PAC end sequence database for sequence-ready map building

JOURNAL Unpublished

COMMENT Contact: de Jong, P.J., Children's Hospital Oakland Research Institute, 747 Fifty-second Street, Oakland, CA 94616, USA. Tel: 510 450 7911 Fax: 510 450 7924 Email: pdejong@mail.cho.org PAC end sequences for clone availability please contact Peter de Jong (pdejong@mail.cho.org). FAX: 510 450 7924 www.choi.org/bacpac Seq primer: 17

Class: PAC end.

FEATURES

source

1..391

location/qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="RNC1-6-171A1017"

/sex="female"

/cell_type="lymphocytes"

/lab_host="E. coli DH10B"

/clone_lib="RNC1-6"

/note="Vector: pPAC4; PAC clones in E. coli DH10B. For PAC library availability, please contact Peter de Jong (BACPACorders@mail.cho.org). Clones may be purchased from BACPAC Resources (www.bori.org/bacpac) or from Research Genetics (info@resgen.com)"

BASE COUNT 128 a 83 c 91 g 89 t

ORIGIN

Query Match 70.0%; Score 18.2; DB 28; Length 391;
Best local similarity 87.0%; Pred. No. 7,80-92;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY 2 CATTATCAGCTAGCAGCTCGAA 24
111111111111111111111111

Db 255 CATTACGACGAGCAGCTTCGA 233

RESULT 11

LOCUS AA760928 462 bp mRNA linear 07-DEC-1998

DEFINITION rnc1-6-171A1017 Homo sapiens genomic clone RNC1-6-171A1017, genomic survey sequence.

ACCESSION AA760928

VERSION AA760928.1 GI:2809858

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 462)

AUTHORS Mammalia, Euteria; Primates; Catarrhini; Hominoidea; Homo.

TITLE Mammalian rnc1-6-171A1017

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@nci.nih.gov
Tissue procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

DEFINITION RNC1 6, 171A1017, RNC1 6 Homo sapiens genomic clone RNC1-6-171A1017, genomic survey sequence.

ACCESSION M0274752

VERSION M0274752.1 GI:1852596

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 391)

AUTHORS Bae, A., Cairo, A., Calabrese, J., Grogawa, K., Van Oost, M., Wu, J. and de Jong, P.J.

TITLE BAC and PAC end sequence database for sequence-ready map building

JOURNAL Unpublished

COMMENT Contact: de Jong, P.J., Children's Hospital Oakland Research Institute, 747 Fifty-second Street, Oakland, CA 94616, USA. Tel: 510 450 7911 Fax: 510 450 7924 Email: pdejong@mail.cho.org PAC end sequences for clone availability please contact Peter de Jong (pdejong@mail.cho.org). FAX: 510 450 7924 www.choi.org/bacpac Seq primer: 17

Class: PAC end.

FEATURES

source

1..391

location/qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="RNC1-6-171A1017"

/sex="female"

/cell_type="lymphocytes"

/lab_host="E. coli DH10B"

/clone_lib="RNC1-6"

/note="Vector: pPAC4; PAC clones in E. coli DH10B. For PAC library availability, please contact Peter de Jong (BACPACorders@mail.cho.org). Clones may be purchased from BACPAC Resources (www.bori.org/bacpac) or from Research Genetics (info@resgen.com)"

BASE COUNT 128 a 83 c 91 g 89 t

ORIGIN

Query Match 70.0%; Score 18.2; DB 28; Length 391;
Best local similarity 87.0%; Pred. No. 7,80-92;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY 2 CATTATCAGCTAGCAGCTCGAA 24
111111111111111111111111

Db 255 CATTACGACGAGCAGCTTCGA 233

RESULT 11

LOCUS AA760928 462 bp mRNA linear 07-DEC-1998

DEFINITION rnc1-6-171A1017 Homo sapiens genomic clone RNC1-6-171A1017, genomic survey sequence.

ACCESSION AA760928

VERSION AA760928.1 GI:2809858

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 462)

AUTHORS Mammalia, Euteria; Primates; Catarrhini; Hominoidea; Homo.

TITLE Mammalian rnc1-6-171A1017

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@nci.nih.gov
Tissue procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

1

2

3

DEFINITION
R261.6.17A1A17 Sept 4 Homo sapiens genomic clone (R261.6.17A1A17)
genomic survey sequence.

ACCESSION
M2274752

VERSION
M2274752.1 GI:3852596

KEYWORDS
GSS.

ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
de Jong, P.J.,
BAC and PAC end sequence database for sequence-ready map including
unpublished
Contact: de Jong, P.J.,
Children's Hospital Oakland Research Institute,
747 Fifty-second Street, Oakland, CA 94609-1609, USA
Tel: 510 450 7911
Fax: 510 450 7924
Email: pdejong@mail.cro.org
PAC end sequences, for clone availability please contact Peter de
Jong (pdejong@mail.cro.org). BAC/PAC Resources WWW site:
www.croli.org/bacpac
Seq primer: T7
Class: PAC end.

FEATURES
SOURCE
Location/Qualifiers
1..491
/organism "Homo sapiens"
/mol_type "genomic DNA"
/db_xref "taxon:9606"
/clone "R261-6-17A1A17"
/sex "female"
/cell_type "lymphocytes"
/lab_host "E. coli DH10B"
/clone_lib "R261.6"
/vector "Vector, pFC24, two clones in pUC19 library, for new
library availability, please contact Peter de Jong
(BAC/PAC orders: mail.cro.org). Clones may be purchased from
BAC/PAC Resources (www.croli.org/bacpac) or from Research
Genetics (info@resgen.com)"

BASE COUNT
128 a 83 c 91 g 89 t

ORIGIN
Query Match: 70.0%; Score 19.2; E=2e-04; Length 491
Best local Similarity: 87.0%; Prod. No. 7.0e-027
Matches 29; Conservative 0; Mismatch 4; Indels 0; Gaps 0

Y
3 TTGGAAGTCTACTGATTAAAG 25
||||| 1111111111111111
DB 243 TTCAACTGCTGCTGTTATAG 255

FEATURES
DEFINITION
AA760928/0
AA760928.1 Ref: NCBI_GSS Homo sapiens EST, partial, from 1988
mRNA sequence.

ACCESSION
AA760928
AA760928.1 GI:2809458

KEYWORDS
EST.

ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Fukui-Yota, Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 462)
NCI-CCP http://www.ncbi.nlm.nih.gov/ncicp
National Cancer Institute, Cancer Genome Annotation Project (2006),
unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@ncbi.nlm.nih.gov
Tissue procurement: Christopher A. McKelvey, M.D., David M. Miller,
Emmett Buck, M.D., Ph.D.

[illegible]

$$\frac{[A]_0 - [N]}{[N]} = \frac{[A]_0}{[N]} - 1$$
[illegible][illegible][illegible][illegible][illegible][illegible]

of the *Journal of the American Medical Association*, 1963; 181: 111-113.

Received 1997-05-21; revised 1997-07-21; accepted 1997-08-01.
© 1998 Blackwell Science Ltd *Journal of Internal Medicine* 243: 111-117

[illegible]

Page 84, 200, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

With the assistance of the following Board of Directors and the www.fishbase.org Web site, we have been able to identify the following 100 fish species that are listed in the IUCN Red List and are found in the Hudson River. Although the Hudson River is not listed as a "critical habitat" for any of these species, the species are listed as "endangered" or "threatened" because of declines in their populations.

Researcher's name: _____
 Date: _____
 Time: _____
 Location: _____
 Weather: _____
 Observations: _____
 Conclusions: _____
 Signature: _____

[illegible][illegible]
$$\begin{aligned} & \text{Zur ersten } {}^n\text{Menge} \\ & \text{Zur zweiten } {}^n\text{Menge} \\ & \text{Zur dritten } {}^n\text{Menge} \\ & \text{Zur vierten } {}^n\text{Menge} \\ & \text{Zur fünften } {}^n\text{Menge} \\ & \text{Zur sechsten } {}^n\text{Menge} \\ & \text{Zur siebten } {}^n\text{Menge} \\ & \text{Zur achten } {}^n\text{Menge} \\ & \text{Zur neunten } {}^n\text{Menge} \\ & \text{Zur zehnten } {}^n\text{Menge} \end{aligned}$$

For the first time, we have shown that the β -phase of the PbTiO_3 is not a simple ferroelectric phase, but a ferroelectric phase with a complex internal structure. The β -phase of PbTiO_3 is a ferroelectric phase with a complex internal structure, and it is not a simple ferroelectric phase. The β -phase of PbTiO_3 is a ferroelectric phase with a complex internal structure, and it is not a simple ferroelectric phase.

[illegible]

5 GAAGTCTAGCTGATTAATCT 26
 11111111111111111111
 92 GAAGTCTAGCTGATTAATCT 112

RESULT 15

LOCUS A1657536/c

DEFINITION A1657536 584 bp mRNA linear EST 05-MAY-1997

ALERTS: Aedes aegypti M. EST/EST Library Aedes aegypti cDNA clone

ACCESSION A1657536

VERSION A1657536.1 GI:4753526

KEYWORDS EST

SOURCE Aedes aegypti (yellow fever mosquito)

ORGANISM Aedes aegypti

REFERENCE Eukaryota; Metazoa; Arthropoda; Insecta; Phlebotomus

AUTHORS Neoptera; Endopterygota; Diptera; Nematocera; Aedes

TITLE Gill, S. S., Ross, L. S., and Madick, H.

Expressed sequence tags of cDNA clones from an enriched Malpighian

tubule and gut library from Aedes aegypti

JOURNAL Unpublished

COMMENT Contact: Gill, S. S.

Environmental Toxicology

University of California, Riverside

5419 Boyce Hall, Riverside, CA 92521, USA

tel: 909 787 3547

Fax: 909 787 3087

Email: sarjeet.gill@ucr.edu

Seq primer: GCAGTCTGATTAATCTGAT

High quality sequence stop: 584

Location/Qualifiers

1..583

/organism "Aedes aegypti"

/mol_type "mRNA"

/db_xref "taxon:7159"

/clone "hd59"

/sex "female"

/issue_type "malpighian tubules and gut"

/dev_stage "adult"

/lab_host "MH10B"

/clone_1lib "Aedes aegypti M. EST/EST Library"

/note "Vector: pSP6B1; Site 1: SalI; Site 2: NotI; the

cDNA was cloned into the SalI/NotI sites of pSP6B1."

BASE COUNT 162 a 130 c 143 g 146 t

ORIGIN

Query Match 68.58; Score 17.8; DB 9; Length 583;

Best local Similarity 90.58; Fred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 GCGTCAGCTGATTAATCT 21

11111111111111111111

549 GCGTCAGCTGATTAATCT 529

Search completed: August 14, 2003, 05:46:45

Job time: 1617.87 secs

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NAME: MATH
 FIRST NAME: MATH
 LAST NAME: MATH
 ADDRESS: 207 CONSUMERS BLVD
 CITY: NEW YORK
 STATE: NY
 ZIP: 10001

RESULTS:

Page 1 of 1

APPLICANT: MATH

APPLICANT: INFORMATION

APPLICANT: INFORMATION: MATH

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APPLICANT: INFORMATION: MATH

APPLICANT: BOSS, J. L.
 TITLE OF INVENTION: METHOD FOR CONTROLLING A VEHICLE
 NUMBER OF CLAIMS: 1
 PATENT NUMBER: 1,000,000
 ADDRESS: 1000 M Street, N.W.
 CITY: Washington, D.C.
 STATE: DISTRICT OF COLUMBIA
 COUNTRY: UNITED STATES OF AMERICA
 DATE: 1998-08-14
 INVENTOR: BOSS, J. L.
 TITLE: METHOD FOR CONTROLLING A VEHICLE
 ABSTRACT: A method for controlling a vehicle, comprising the steps of: receiving a signal from a sensor; processing the signal; and controlling the vehicle based on the processed signal.
 CLAIMS: 1. A method for controlling a vehicle, comprising the steps of: receiving a signal from a sensor; processing the signal; and controlling the vehicle based on the processed signal.
 DESCRIPTION: The present invention relates to a method for controlling a vehicle. More specifically, the present invention relates to a method for controlling a vehicle based on a signal received from a sensor. The method of the present invention includes the steps of: receiving a signal from a sensor; processing the signal; and controlling the vehicle based on the processed signal. The sensor may be any type of sensor, such as a temperature sensor, a pressure sensor, a motion sensor, or a position sensor. The method of the present invention may be used in a variety of applications, such as in a vehicle, a machine, or a system.

Query Match 65.7% Score 18.4 Lb 4 Length 678
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22 Conservative 0 Mismatches 6 Sub 10 0 Gaps 0

UY 1 CGGCGACCTTAAGAAAGCTTCGACAGG 28
 ||| ||||| || ||| ||||| ||
 DB 343 CGGCGACCTGACGACAGCTTCGACAGG 316

RESULT 6
 US-09-252-991A-1512
 Sequence 1512: Aff11-27-1998 us09252991a

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252-991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1512

LENGTH: 1416

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1512

Query Match 65.7% Score 18.4 Lb 4 Length 1416
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22 Conservative 0 Mismatches 6 Sub 10 0 Gaps 0

UY 1 CGGCGACCTTAAGAAAGCTTCGACAGG 28
 ||| ||||| || ||| ||||| ||
 DB 851 CGGCGACCTGACGACAGCTTCGACAGG 878

RESULT 7

US-09-252-991A-1464
 Sequence 1464: Application us09252991a

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252-991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1464

LENGTH: 2352

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1464

Query Match 65.7% Score 18.4 Lb 4 Length 2352
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22 Conservative 0 Mismatches 6 Sub 10 0 Gaps 0

UY 1 CGGCGACCTTAAGAAAGCTTCGACAGG 28
 ||| ||||| || ||| ||||| ||
 DB 807 CGGCGACCTGACGACAGCTTCGACAGG 834

RESULT 8
 US-09-252-991A-1663/C

Sequence 1663: Application us09252991a

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252-991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1663

LENGTH: 1429

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1663

Query Match 65.7% Score 18.4 Lb 4 Length 1429
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22 Conservative 0 Mismatches 6 Sub 10 0 Gaps 0

UY 1 CGGCGACCTTAAGAAAGCTTCGACAGG 28
 ||| ||||| || ||| ||||| ||
 DB 1429 CGGCGACCTGACGACAGCTTCGACAGG 1459

RESULT 9

US-09-252-991A-1663/C

Sequence 1663: Application us09252991a

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252-991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1663

LENGTH: 1429

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1663/C

Sequence 1663: Application us09252991a

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252-991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1663

LENGTH: 1429

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1663/C

Sequence 1663: Application us09252991a

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252-991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1663

LENGTH: 1429

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1663/C

SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US96-09536-1 083
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 46, 473
 REFERENCE/POCKET NUMBER: FR449P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (401) 309-8512
 INTERACTION FOR SEQ ID NO. 139:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 805 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-961-083-139

Query Match: 61.5% Score 16, 18 % Identity 60%
 Host Local Similarity 79.2% Pred. No. 79
 Matches 19: Conservative 0: Mismatches 5: Indels 0: Gaps 0

QY 2 CATTATAGCTAGCTAGCTTAGC 25
 DB 629 CATTATAGCTAGCTAGCTTAGC 652

RESULT 12
 US-09-536-784-139
 Sequence 139: Application US/095-0784
 Patent No. 6573082
 GENERAL INFORMATION:
 APPLICANT: Choi et al
 TITLE OF INVENTION: Methods for determining Antigenic and Viral
 NUMBER OF SEQUENCES: 452
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44M storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 09-536-784
 FILING DATE: 30-04-1997
 CLASSIFICATION: unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/961,083
 FILING DATE: 01-10-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Michelle S. Marks
 REGISTRATION NUMBER: 41,971
 REFERENCE/POCKET NUMBER: FR449P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 149:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 805 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 139:

US-09-536-784-139
 Query Match: 61.5% Score 16, 18 % Identity 60%
 Host Local Similarity 79.2% Pred. No. 79
 Matches 19: Conservative 0: Mismatches 5: Indels 0: Gaps 0

QY 2 CATTATAGCTAGCTAGCTTAGC 25
 DB 629 CATTATAGCTAGCTAGCTTAGC 652

RESULT 13
 US-96-09536-139
 Sequence 452: Application US/095-0784
 Patent No. 6573082
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences
 TITLE OF INVENTION: Methods for determining Antigenic and Viral
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44M storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 96-09536-139
 FILING DATE: 30-04-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/961,083
 FILING DATE: 01-10-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Michelle S. Marks
 REGISTRATION NUMBER: 41,971
 REFERENCE/POCKET NUMBER: FR449P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 149:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 805 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-96-09536-139

Query Match: 61.5% Score 16, 18 % Identity 60%
 Host Local Similarity 79.2% Pred. No. 79
 Matches 19: Conservative 0: Mismatches 5: Indels 0: Gaps 0

QY 2 CATTATAGCTAGCTAGCTTAGC 25
 DB 629 CATTATAGCTAGCTAGCTTAGC 652

US 10 009 962 4

10 009 962 4

10 009 962 4

RESULT 1

US 10 009 962 4

Patent No. 6,500,016

GENERAL INFORMATION:

APPLICANT: Alan D. Brown

APPLICANT: Kenneth P. Brown

APPLICANT: John H. Brown

TITLE OF INVENTION: METHOD FOR DETERMINING THE RELATIONSHIP OF ANIMALS TO OTHER ANIMALS

TITLE OF INVENTION: METHOD FOR DETERMINING THE RELATIONSHIP OF ANIMALS TO OTHER ANIMALS

NUMBER OF INVENTION: 10

ADDRESS: 10000 N. 10th St., Suite 100, West Lake, Arizona, 85361-1000

STATE: WA (Washington)

CITY: Seattle

COUNTRY: United States of America

DATE: 08/14/03

INVENTOR: Alan D. Brown

INVENTOR: Kenneth P. Brown

INVENTOR: John H. Brown

OPERATING SYSTEM: Windows 98

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/000,000

FILED DATE: 27 May 2003

CLASSIFICATION:

APPLICATION NUMBER: 08/000,000

FILED DATE: 08/14/03

CLASSIFICATION:

NAME: Brown, Alan D.

REFERENCE NUMBER: 6,500,016

REFERENCE NUMBER: 6,500,016

REFERENCE NUMBER: 6,500,016

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REFERENCE NUMBER: 6,500,016

REFERENCE NUMBER: 6,500,016

REFERENCE NUMBER: 6,500,016

REFERENCE NUMBER: 6,500,016

REFERENCE NUMBER: 6,500,016

RESULT 12

US-10-288-930-1/6
 : Sequence 1, Application US/0208030
 : Publication No. US2003028822A1
 : GENERAL INFORMATION:
 : APPLICANT: Glenn, Matthew
 : APPLICANT: Lubbers, Mark W
 : APPLICANT: Dekker, James
 : TITLE OF INVENTION: Poly-oligo-oligos and polypeptides, materials incorporating
 : FILE REFERENCE: 11000 10490161
 : CURRENT APPLICATION NUMBER: US/0208030
 : PRIOR FILING DATE: 2002-11-05
 : PRIOR APPLICATION NUMBER: 09/721,623
 : PRIOR FILING DATE: 2000-11-28
 : PRIOR APPLICATION NUMBER: 60/418,801
 : NUMBER OF SEQ ID NOS: 124
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO: 1
 : LENGTH: 711
 : TYPE: DNA
 : ORGANISM: Lactobacillus rhamnosus
 US-10-288-930-1

Query Match 65.48; Score 17; DB 12; Length 711;
 Best Local Similarity 80.08; Pred. No. 2,3e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CATTGCAAGTCTAGCTAGTATATG 25
 DB 465 CATTGCAAGTCTAGCTAGTATATG 441

RESULT 13

US-09-822-849A-247
 : Sequence 247, Application US/09022849A
 : Patent No. US20030045170A1
 : GENERAL INFORMATION:
 : APPLICANT: Wong, Gordon G.
 : APPLICANT: Clark, Hilary
 : APPLICANT: Frechel, Kim
 : APPLICANT: Agostino, Michael J.
 : APPLICANT: Howes, Steven H.
 : APPLICANT: Resnick, Richard J.
 : APPLICANT: Gulukota, Kamalakar
 : APPLICANT: Graham, James R.
 : TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
 : FILE REFERENCE: GIN 6403
 : CURRENT APPLICATION NUMBER: US/09022849A
 : CURRENT FILING DATE: 2001-09-04
 : PRIOR APPLICATION NUMBER: 60/195,582
 : PRIOR FILING DATE: 2000-04-05
 : NUMBER OF SEQ ID NOS: 598
 : SOFTWARE: Patent in Ver. 2.0
 : SEQ ID NO: 247
 : LENGTH: 2254
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-09-822-849A-247

Query Match 65.48; Score 17; DB 9; Length 2254;
 Best Local Similarity 90.09; Pred. No. 2,9e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CATTGCAAGTCTAGCTAGTATATG 25
 DB 563 CATTGCAAGTCTAGCTAGTATATG 587

RESULT 14

US-09-764-891-9927/6
 : Sequence 9927, Application US/09764891
 : Publication No. US2003007688A1
 : GENERAL INFORMATION:
 : APPLICANT: Kosco et al.
 : TITLE OF INVENTION: Methods of identifying, producing, and administering
 : FILE REFERENCE: 19006
 : CURRENT APPLICATION NUMBER: US/09764891
 : CURRENT FILING DATE: 2001-01-17
 : PRIOR APPLICATION DATA REMOVED - CONSULT FAIM OF FILE WRAPPER
 : NUMBER OF SEQ ID NOS: 19231
 : SOFTWARE: Patent in Ver. 2.0
 : SEQ ID NO: 9927
 : LENGTH: 22237
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-09-764-891-9927

Query Match 65.48; Score 17; DB 12; Length 22237;
 Best Local Similarity 80.08; Pred. No. 4,6e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CTTTCAAGTCTAGCTAGTATATG 25
 DB 564 CTTTCAAGTCTAGCTAGTATATG 540

RESULT 15

US-09-764-891-9926/6
 : Sequence 9926, Application US/09764891
 : Publication No. US2003007688A1
 : GENERAL INFORMATION:
 : APPLICANT: Kosco et al.
 : TITLE OF INVENTION: Methods of identifying, producing, and administering
 : FILE REFERENCE: 19006
 : CURRENT APPLICATION NUMBER: US/09764891
 : CURRENT FILING DATE: 2001-01-17
 : PRIOR APPLICATION DATA REMOVED - CONSULT FAIM OF FILE WRAPPER
 : NUMBER OF SEQ ID NOS: 19231
 : SOFTWARE: Patent in Ver. 2.0
 : SEQ ID NO: 9926
 : LENGTH: 22238
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-09-764-891-9926

Query Match 65.48; Score 17; DB 12; Length 22238;
 Best Local Similarity 80.08; Pred. No. 4,6e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CTTTCAAGTCTAGCTAGTATATG 25
 DB 565 CTTTCAAGTCTAGCTAGTATATG 541

Search completed: August 14, 2003, 09:10:36
 Job Time: 412.152 secs



Source version 5.1.6
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nom nucleic-acid search, using sw model

Run on: August 14, 2003, 02:18:26, started time 470.130, end 470.435

143.016 Million cell updates/second

US-10-009-562-1

Sequence: 1 GCTCGAGCAAGCTTTTAAAGGTGACCG 2H

Scoring table: IDENTITY_NUC

Searched: 1504479 seqs, 1118970152 residues

Total number of hits satisfying chosen parameters: 3000000

Minimum Eff. Seq. Length: 0

Maximum Match: 100%

Database : published_applications_NA:

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Quality	Match	Length	DB	ID	Insert	Ref	Path
1	28	100.0	28	14	08-10-094-944-1		Sequence 1, Affili		
2	28	100.0	28	14	08-10-094-944-1		Sequence 2, Affili		
3	19.5	70.0	245	10	08-09-878-674-7664		Sequence 1, Affili		
4	19.5	70.0	251	10	08-09-878-674-7664		Sequence 2, Affili		
5	19.5	70.0	278	10	08-09-878-674-7664		Sequence 3, Affili		
6	19.5	70.0	7142	9	08-09-922-654-1		Sequence 1, Affili		
7	19.6	70.0	7142	9	08-09-922-654-1		Sequence 2, Affili		
8	19.2	68.6	7127	9	08-08-779-457-16A-7		Sequence 1, Affili		
9	19.4	67.9	1537	10	08-09-924-100-2,296		Sequence 1, Affili		
10	18.8	65.7	1299	9	08-09-939-41-26-1673		Sequence 1, Affili		
11	18.4	65.7	1380	9	08-09-939-41-26-1673		Sequence 2, Affili		
12	18.2	65.0	1295	9	08-09-939-41-26-1673		Sequence 3, Affili		
13	18.2	65.0	3305400	10	08-09-736-624-1		Sequence 1, Affili		
14	18	64.2	238	10	08-09-878-674-7664		Sequence 1, Affili		
15	18	64.2	287	10	08-09-878-674-7664		Sequence 2, Affili		
16	18	64.3	306	10	08-09-878-674-7664		Sequence 3, Affili		

[illegible]

100

$$\begin{aligned} \mathbb{E}[S_{\mathbf{t}}^2] &= 1 \\ \mathbb{E}[S_{\mathbf{t}}] &= 0 \end{aligned}$$

Figure 1 is a schematic representation of the experimental design. It shows a flowchart with the following steps: 1. Selection of 1000 subjects, 2. Random assignment to two groups (500 each), 3. Pre-test, 4. Training (10 days), 5. Post-test, 6. Follow-up (10 days), 7. Post-follow-up. The groups are labeled 'Group 1' and 'Group 2'.

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

[illegible][illegible]

THE NEW YORK PUBLIC LIBRARY
ASTOR LENOX TILDEN FOUNDATIONS
500 FIFTH AVENUE
NEW YORK 10017

André Breton, *Le Manifeste du surréalisme*, 1924, in *Œuvres complètes*, Paris, 1964, t. 1, p. 10.

CITY: Seattle
STATE: WA (Washington)
COUNTRY: United States

[illegible]

Minimum: 1 year
Maximum: 10 years

OPERATING SYSTEM: Windows

[illegible]

FINANCIAL

Abstract

2019-2020

THE NEW YORK PUBLIC LIBRARY

ANNALS

[illegible]

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Chlorophyll c* (Chl *c*)
 4. *Chlorophyll d* (Chl *d*)
 5. *Chlorophyll e* (Chl *e*)
 6. *Chlorophyll f* (Chl *f*)
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 8. *Chlorophyll h* (Chl *h*)
 9. *Chlorophyll i* (Chl *i*)
 10. *Chlorophyll j* (Chl *j*)
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 97. *Chlorophyll arz* (Chl *arz*)
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 117. *Chlorophyll akz* (Chl *akz*)
 118. *Chlorophyll alz* (Chl *alz*)
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 120. *Chlorophyll anz* (Chl *anz*)
 121. *Chlorophyll aoz* (Chl *aoz*)
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 123. *Chlorophyll aqz* (Chl *aqz*)
 124. *Chlorophyll arz* (Chl *arz*)
 125. *Chlorophyll asz* (Chl *asz*)
 126. *Chlorophyll atz* (Chl *atz*)
 127. *Chlorophyll auz* (Chl *auz*)
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 131. *Chlorophyll ayz* (Chl *ayz*)
 132. *Chlorophyll ayz* (Chl *ayz*)
 133.

100

US-09-878-574-13495/C
Sequence 1495, Application US/09678574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael B.
TITLE OF INVENTION: Nucleic Acid Molecules and Their Use in Gene Assays and Cell
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(1540)B
CURRENT APPLICATION NUMBER: US/09678574
CURRENT FILING DATE: 2001-12-21
PRIORITY APPLICATION NUMBER: 09/733,535
PRIORITY FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO: 1495
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Cloned for 70195726FBI
US-09-878-574-13495

Query Match: 70.0% Score 19.6; DB Len: Length 7142
Best Local Similarity: 84.6% Pred. No: 172
Matches: 22; Conserved: 0; Mismatches: 1; Indels: 0

QY 2 CCGCAGAGCTTCTTAAATTCGAG 27

DB 153 CCGCAGAGCTTCTTAAATTCGAG 128

RESULT 5
US-09-927-616A-1/C
Sequence 1, Application US/09927616A
Patent No. US2002099354A1
GENERAL INFORMATION:
APPLICANT: Triplett, Eric W.
APPLICANT: Herliach, Thomas G.
TITLE OF INVENTION: Biological Control of Crown Gall Disease
FILE REFERENCE: 660256-97273
CURRENT APPLICATION NUMBER: US/09927616A
CURRENT FILING DATE: 2001-11-02
PRIORITY APPLICATION NUMBER: 60/274,630
PRIORITY FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patonlin Ver. 2.1
SEQ ID NO: 1
LENGTH: 7142
TYPE: DNA
ORGANISM: Klebsiella pneumoniae for 1413111
FEATURES:
NAME/KEY: CDS
LOCATION: (597)..(722)
OTHER INFORMATION: tRNA coding sequence
NAME/KEY: CDS
LOCATION: (794)..(1912)
OTHER INFORMATION: tRNA coding sequence
NAME/KEY: CDS
LOCATION: (2982)..(4229)
OTHER INFORMATION: tRNA coding sequence
NAME/KEY: CDS
LOCATION: (4968)..(5741)
OTHER INFORMATION: tRNA coding sequence
NAME/KEY: CDS
LOCATION: (5966)..(6778)
OTHER INFORMATION: tRNA coding sequence
US-09-927-616A-1

Query Match: 70.0% Score 19.6; DB Len: Length 7142
Best Local Similarity: 84.6% Pred. No: 172
Matches: 22; Conserved: 0; Mismatches: 1; Indels: 0

QY 4 CCGCAGAGCTTCTTAAATTCGAG 28

US-09-927-616A-1/C

RESULT 7
US-09-927-616A-1/C
Sequence 7, Application US/09927616A
Patent No. US2002099354A1
GENERAL INFORMATION:
APPLICANT: Triplett, Eric W.
APPLICANT: Herliach, Thomas G.
TITLE OF INVENTION: Biological Control of Crown Gall Disease
FILE REFERENCE: 660256-97273
CURRENT APPLICATION NUMBER: US/09927616A
CURRENT FILING DATE: 2001-11-02
PRIORITY APPLICATION NUMBER: 60/274,630
PRIORITY FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patonlin Ver. 2.1
SEQ ID NO: 7
LENGTH: 7142
TYPE: DNA
ORGANISM: Klebsiella pneumoniae for 1413111
FEATURES:
NAME/KEY: CDS
LOCATION: (1908)..(2979)
OTHER INFORMATION: tRNA coding sequence
NAME/KEY: CDS
LOCATION: (421)..(1400)
OTHER INFORMATION: tRNA coding sequence
US-09-927-616A-1

Query Match: 70.0% Score 19.6; DB Len: Length 7142
Best Local Similarity: 84.6% Pred. No: 172
Matches: 22; Conserved: 0; Mismatches: 1; Indels: 0

QY 4 CCGCAGAGCTTCTTAAATTCGAG 28

DB 153 CCGCAGAGCTTCTTAAATTCGAG 128

RESULT 8
US-09-927-616A-1/C
Sequence 8, Application US/09927616A
Patent No. US2002099354A1
GENERAL INFORMATION:
APPLICANT: Triplett, Eric W.
APPLICANT: Herliach, Thomas G.
TITLE OF INVENTION: Biological Control of Crown Gall Disease
FILE REFERENCE: 660256-97273
CURRENT APPLICATION NUMBER: US/09927616A
CURRENT FILING DATE: 2001-11-02
PRIORITY APPLICATION NUMBER: 60/274,630
PRIORITY FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patonlin Ver. 2.1
SEQ ID NO: 8
LENGTH: 7142
TYPE: DNA
ORGANISM: Klebsiella pneumoniae for 1413111
FEATURES:
NAME/KEY: CDS
LOCATION: (1908)..(2979)
OTHER INFORMATION: tRNA coding sequence
NAME/KEY: CDS
LOCATION: (421)..(1400)
OTHER INFORMATION: tRNA coding sequence
US-09-927-616A-1

RESULT 12

US-09-738-626-1692
 : Sequence: 1592, Application: US/99/738-626
 : Publication No.: US20020197605A1
 : GENERAL INFORMATION:
 : APPLICANT: NAKAGAWA, SATOSHI
 : APPLICANT: MIZOGUCHI, HIROSHI
 : APPLICANT: AMDO, SEIKO
 : APPLICANT: HAYASHI, MIKIO
 : APPLICANT: OCHIAI, KEIKO
 : APPLICANT: YOKOI, HARUHIKO
 : APPLICANT: TATEISHI, AKIHIRO
 : APPLICANT: SENO, AKIHIRO
 : APPLICANT: IKEDA, MASARU
 : APPLICANT: OZAKI, AKIO
 : TITLE OF INVENTION: NOVEL PEPTIDE-INDUCED
 : FILE REFERENCE: 249-125
 : CURRENT APPLICATION NUMBER: US-99/738-626
 : CURRENT FILING DATE: 2000-12-18
 : PRIOR APPLICATION NUMBER: JP 99/777184
 : PRIOR FILING DATE: 1999-12-16
 : PRIOR APPLICATION NUMBER: JP 99/159162
 : PRIOR FILING DATE: 2000-04-07
 : PRIOR APPLICATION NUMBER: JP 99/299938
 : PRIOR FILING DATE: 2000-09-03
 : NUMBER OF SEQ ID NOS: 7059
 : SOFTWARE: Patent In Ver. 3.0
 : SEQ ID NO: 1692
 : TYPE: DNA
 : LENGTH: 1296
 : ORGANISM: Corynebacterium glutamicum
 : US-09-738-626-1692

Query Match 65.08% Score 18.21 Length 1296
 Best Local Similarity 87.08% Pred. No. 67
 Matches 20 Conserved 0 of Mismatches 21 Indels 0 Gaps 0
 Y 2 CCGGAGAGGCTTCTAGGTCG 24
 H 622 CCGGAGAGGCTTCTAGGTCG 844

RESULT 13

US-09-738-626-1692
 : Sequence: 1, Application: US/99/738-626
 : Publication No.: US20020197605A1
 : GENERAL INFORMATION:
 : APPLICANT: NAKAGAWA, SATOSHI
 : APPLICANT: MIZOGUCHI, HIROSHI
 : APPLICANT: AMDO, SEIKO
 : APPLICANT: HAYASHI, MIKIO
 : APPLICANT: OCHIAI, KEIKO
 : APPLICANT: YOKOI, HARUHIKO
 : APPLICANT: TATEISHI, AKIHIRO
 : APPLICANT: SENO, AKIHIRO
 : APPLICANT: IKEDA, MASARU
 : APPLICANT: OZAKI, AKIO
 : TITLE OF INVENTION: NOVEL PEPTIDE-INDUCED
 : FILE REFERENCE: 249-125
 : CURRENT APPLICATION NUMBER: US-99/738-626
 : CURRENT FILING DATE: 2000-12-18
 : PRIOR APPLICATION NUMBER: JP 99/777184
 : PRIOR FILING DATE: 1999-12-16
 : PRIOR APPLICATION NUMBER: JP 99/159162
 : PRIOR FILING DATE: 2000-04-07
 : PRIOR APPLICATION NUMBER: JP 99/299938
 : PRIOR FILING DATE: 2000-09-03
 : NUMBER OF SEQ ID NOS: 7059
 : SOFTWARE: Patent In Ver. 3.0
 : SEQ ID NO: 1
 : LENGTH: 3309400

TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-1

Query Match 65.08% Score 18.21 Length 1296
 Best Local Similarity 87.08% Pred. No. 67
 Matches 20 Conserved 0 of Mismatches 21 Indels 0 Gaps 0
 Y 2 CCGGAGAGGCTTCTAGGTCG 24
 H 622 CCGGAGAGGCTTCTAGGTCG 844

RESULT 14

US-09-878-574-8642/0
 : Sequence: 8642, Application: US/ 99/878-574
 : Patent No.: US20020197605A1
 : GENERAL INFORMATION:
 : APPLICANT: Thompson, Richard L.
 : APPLICANT: Thompson, Richard L.
 : TITLE OF INVENTION: NOVEL PEPTIDE-INDUCED
 : FILE REFERENCE: 249-125
 : CURRENT APPLICATION NUMBER: US-99/878-574
 : CURRENT FILING DATE: 2000-12-18
 : PRIOR APPLICATION NUMBER: JP 99/777184
 : PRIOR FILING DATE: 1999-12-16
 : PRIOR APPLICATION NUMBER: JP 99/159162
 : PRIOR FILING DATE: 2000-04-07
 : NUMBER OF SEQ ID NOS: 7059
 : SOFTWARE: Patent In Ver. 3.0
 : SEQ ID NO: 8642
 : TYPE: DNA
 : LENGTH: 1296
 : ORGANISM: Corynebacterium glutamicum
 : OTHER INFORMATION: 100% identical to US-09-738-626-1692
 : US-09-878-574-8642

Query Match 65.08% Score 18.21 Length 1296
 Best Local Similarity 87.08% Pred. No. 67
 Matches 21 Conserved 0 of Mismatches 21 Indels 0 Gaps 0
 Y 2 CCGGAGAGGCTTCTAGGTCG 24
 H 622 CCGGAGAGGCTTCTAGGTCG 844

RESULT 15

US-09-878-574-8642/0
 : Sequence: 8642, Application: US/ 99/878-574
 : Patent No.: US20020197605A1
 : GENERAL INFORMATION:
 : APPLICANT: Thompson, Richard L.
 : APPLICANT: Thompson, Richard L.
 : TITLE OF INVENTION: NOVEL PEPTIDE-INDUCED
 : FILE REFERENCE: 249-125
 : CURRENT APPLICATION NUMBER: US-99/878-574
 : CURRENT FILING DATE: 2000-12-18
 : PRIOR APPLICATION NUMBER: JP 99/777184
 : PRIOR FILING DATE: 1999-12-16
 : PRIOR APPLICATION NUMBER: JP 99/159162
 : PRIOR FILING DATE: 2000-04-07
 : NUMBER OF SEQ ID NOS: 7059
 : SOFTWARE: Patent In Ver. 3.0
 : SEQ ID NO: 8642
 : TYPE: DNA
 : LENGTH: 1296
 : ORGANISM: Corynebacterium glutamicum
 : OTHER INFORMATION: 100% identical to US-09-738-626-1692
 : US-09-878-574-8642

Query Match 65.08% Score 18.21 Length 1296
 Best Local Similarity 87.08% Pred. No. 67
 Matches 21 Conserved 0 of Mismatches 21 Indels 0 Gaps 0
 Y 2 CCGGAGAGGCTTCTAGGTCG 24
 H 622 CCGGAGAGGCTTCTAGGTCG 844

Thu Aug 14 09:09:34 2003

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Page 6

1. $\mathcal{A} = \{A_1, A_2, \dots, A_n\}$ is a family of sets.

Theorem 6. Let $\{A_i\}_{i=0}^{\infty}$ be a sequence of matrices satisfying

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YILMAZ
ÖZDEMİR
EVA
NADİ ÖZALP
DOKTORA İHTİSAP

Thu Aug 14 09:09:37 2003

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Page 6

[illegible]

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DOI: 10.1177/1056492607306565
<http://jmi.sagepub.com>

RESULT 12

US-10-288-930-1
 ? Sequence 9927, Application 65/724,623
 ? Publication No. US2002013982A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Glenn, Matthew
 ? APPLICANT: Lubberts, Mark W
 ? APPLICANT: Decker, James
 ? TITLE OF INVENTION: Polymers, lactides and poly(l-lactides) and poly(l-lactides) incorporation
 ? FILE REFERENCE: 11000,1048ulcl
 ? CURRENT APPLICATION NUMBER: 75,724,623
 ? PRIOR FILING DATE: 2002-11-05
 ? PRIOR FILING DATE: 2000-11-28
 ? PRIOR APPLICATION NUMBER: 66/743,801
 ? PRIOR FILING DATE: 1999-12-02
 ? NUMBER OF SEQ ID NOS: 124
 ? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO: 1
 ? LENGTH: 711
 ? TYPE: DNA
 ? ORGANISM: Lactobacillus rhamnosus
 US-10-288-930-1

Query Match

Best Local Similarity 65.4%; Score 17; Db 12; Length 711
 Best Local Similarity 80.0%; Prod. No. 2,80-02

Matches 20; Conservative 9; Mismatches 5; Indels 0; Gaps 0

QY 2 CATTATCAGTACGACTGACCTGAAAG 26
 DB 441 CATTATCAGTACGACTGACCTGAAAG 465

RESULT 13

US-09-822-919A 247/2
 ? Sequence 247, Application 66/743,801
 ? Patent No. US20020045170A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Wong, Gordon C.
 ? APPLICANT: Clark, Hilary
 ? APPLICANT: Freckel, Kim
 ? APPLICANT: Apostolov, Michael J.
 ? APPLICANT: Howes, Steven H.
 ? APPLICANT: Resnick, Richard J.
 ? APPLICANT: Galkota, Kamalakar
 ? APPLICANT: Graham, James R.
 ? TITLE OF INVENTION: POLYMERIZATION ENHANCING N-VEL SHOTTER PROTEINS
 ? FILE REFERENCE: GIN 6403
 ? CURRENT APPLICATION NUMBER: 66/743,801
 ? PRIOR FILING DATE: 2001-09-04
 ? PRIOR APPLICATION NUMBER: 60/195,582
 ? PRIOR FILING DATE: 2000-04-05
 ? NUMBER OF SEQ ID NOS: 598
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 247
 ? LENGTH: 2254
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-822-919A-247

Query Match

Best Local Similarity 65.4%; Score 17; Db 12; Length 2254
 Best Local Similarity 80.0%; Prod. No. 2,80-02

Matches 20; Conservative 9; Mismatches 5; Indels 0; Gaps 0

QY 2 CATTATCAGTACGACTGACCTGAAAG 26
 DB 587 CATTATCAGTACGACTGACCTGAAAG 564

RESULT 14

US-09-764-891 9926
 ? Sequence 9926, Application 65/724,623
 ? Publication No. US2002013982A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Rosen, et al.
 ? TITLE OF INVENTION: Nucleotide Analogs, Phosphates, and Analogues
 ? FILE REFERENCE: 11000,1048ulcl
 ? CURRENT APPLICATION NUMBER: 75,724,623
 ? PRIOR FILING DATE: 2002-11-05
 ? PRIOR FILING DATE: 2000-11-28
 ? PRIOR APPLICATION NUMBER: 66/743,801
 ? NUMBER OF SEQ ID NOS: 124
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 9927
 ? LENGTH: 2254
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-764-891 9926

Query Match

Best Local Similarity 65.4%; Score 17; Db 14; Length 2254
 Best Local Similarity 80.0%; Prod. No. 2,80-02

Matches 20; Conservative 9; Mismatches 5; Indels 0; Gaps 0

QY 1 CATTATCAGTACGACTGACCTGAAAG 26
 DB 966 CATTATCAGTACGACTGACCTGAAAG 964

RESULT 15

US-09-764-891 9926
 ? Sequence 9926, Application 65/724,623
 ? Publication No. US2002013982A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Rosen, et al.
 ? TITLE OF INVENTION: Nucleotide Analogs, Phosphates, and Analogues
 ? FILE REFERENCE: 11000,1048ulcl
 ? CURRENT APPLICATION NUMBER: 75,724,623
 ? PRIOR FILING DATE: 2002-11-05
 ? PRIOR FILING DATE: 2000-11-28
 ? PRIOR APPLICATION NUMBER: 66/743,801
 ? NUMBER OF SEQ ID NOS: 124
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 9926
 ? LENGTH: 2254
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-764-891 9926

Query Match

Best Local Similarity 65.4%; Score 17; Db 14; Length 2254
 Best Local Similarity 80.0%; Prod. No. 2,80-02

Matches 20; Conservative 9; Mismatches 5; Indels 0; Gaps 0

QY 1 CATTATCAGTACGACTGACCTGAAAG 26
 DB 966 CATTATCAGTACGACTGACCTGAAAG 964

Search completed August 14, 2003 11:00 AM
 Job Time: 414.862 secs

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